

FIGURE 1

A. CTTATCGATACCGTCGAAACTTGTATTGCAGCTATAATGGTTACAAATAAAGCAATAGCAT
CACAAATTTCACAAATAAAGCATTTCAGCTACTGCATTCTAGTTGTGGTTGTCAAACTCATCA
+
ATGTATCTTATCATGTC **(Seq ID NO:1)** Cleavage site

B.
A horizontal line represents the DNA sequence. Above it, the sequence "AAAAAA" is written, followed by five vertical plus signs (+) indicating upstream and downstream cleavage-polyadenylation elements. To the right of the sequence is the nucleotide "GCA".

C.
A horizontal line represents the DNA sequence. Above it, the sequence "GCAaaaaaaaaaaaaaaa" is written, followed by five vertical plus signs (+) indicating upstream and downstream cleavage-polyadenylation elements. To the right of the sequence is the label "(Seq ID NO:18)".

+ Upstream and downstream
cleavage- polyadenylation elements



FIGURE 2

► ITR

| | | | | | | |
|-------------|-------------|------------|-------------|-------------------|----------------------|-----|
| CATCATCAAT | AATATACCTT | ATTTGGATT | GAAGCCAATA | TGATAATGAG | GGGGTGGAGT | 60 |
| TTGTGACGTG | GCGCGGGCGG | TGGGAACGGG | GC GGGTGACG | TAGTAGTGTG | <u>GC GGGAAAGTGT</u> | 120 |
| GATGTGCAA | GTGTGGCGGA | ACACATGTAA | CGCAGCGATG | <u>TGGCAAAAGT</u> | GAC G TTTTG | 180 |
| GTGTGCGCCG | GTGTACACAG | GAAGTGACAA | TTTCGCGCG | GT TTTAGCGC | <u>GATGTGTA</u> | 240 |
| TAAATTTGGG | CGTAACCGAG | TAAGATTGG | CCATTTCGCG | GGAAAACTG | AATAAGAGGA | 300 |
| AGTGAAATCT | GAATAATTIT | GTGTACTICA | TAGCGCGTAA | <u>TATTTGTCTA</u> | GGGCCCGGG | 360 |
| GACITITGACC | GTITACGTGG | AGACTCGCCC | AGGIGTTTTT | CTCAGGTGTT | TTC CGC GTTC | 420 |
| CGGGTCAAAG | TTGGCGTTTT | ATTATTATAG | TCAGCTGACG | <u>TGTACTGTAT</u> | TTA TAC CCGG | 480 |
| TGAGTTCCTC | AAGAGGCCAC | TCTTGAGTGC | CAGCGAGTAG | AGTITTCCTCC | TCC GAG CGGC | 540 |
| TCCGACACCG | GGACTGAAA A | TGAGACATAT | TATCTGCCAC | GGAGGTGTTA | TTACCGAAGA | 600 |

• Enhancer elements  dl 103-551 Ar6
 X E2F-motif  dl 189-551
 + Packaging elements  dl 357-551 Ar5

(SEQ ID NO:2)



FIGURE 3A

1 CATCATCAATAATACCTTATTGGATTGAAGCCAATATGATAATGAGGGGTCGAGT
+----- ITR -----+

61 TTGTGACGTGGCGGGGGCGTGGAACCGGGGCGGTGACGTAGGGCGCATCAAGCTTAT
+----- ITR -----+ +-----

121 CGATACCGTCGAACTITGTTTATGAGCTTATAATGGTACAAATAAGCAATAGCATIC
----- polyA -----

181 ACAAAATTCACAAATAAAGCATTTCACTGCATTCTAGTTGTGGTTGTCCAAACTC
----- polyA -----

241 ATCAATGTATCTTATCATGTCTGGATCCGCGCGCTAGCGATCATCCGACAAAGCTGC
----- + +-----

301 GCGCCGCCGCCGCCGCCATTGGCGTACCGCCCCGCCGCCGCCATCTGCCCTCG
----- E2F-1 promoter -----

361 CGCGCGGTCCGGCCGTTAAAGCCAATAGGAACCGCCGCCGTGTTCCCGTCACGCCG
----- E2F-1 promoter -----

421 GGGCAGCCAATTGTGGCGGCGCTGGCGCTCGTGGCTTTCGCGGAAAAGGATTG
----- E2f-1 promoter -----

481 GCGCGTAAAAGTGGCGGACATTGCGAGCGGGGGGGGGGGAGCGGGATCGAG
----- E2f-1 promoter -----

541 CCCTCGATGATATCAGATCATCGGATCCCGGTCGACTGAAAATGAGACATATTATCTGCC
----- + +-----

601 ACGGAGGTGTTATTACCGAAGAAATGGCGGCCAGTCTTTGGACCAGCTGATCGAAGAGG
----- Ela gene -----

661 TACTGGCTGATAATCTTCCACCTCTAGCCATTGAAACCACCTACCCCTCACGAACTGT
----- Ela gene -----

721 ATGATTTAGACGTGACGGCCCCGAAGATCCAACGAGGAGGAGGCGTTCGCAGATTTC
----- Ela gene -----

781 CCGACTCTGTAATGTTGGCGGTGAGGAAGGGATTGACTTACTCACTTTCCGCGCGC
----- Ela gene -----

841 CCGGTTCTCCGGAGCGCCTCACCTTCCGGCAGCCGAGCAGCCGGAGCAGAGGCCT
----- Ela gene -----

901 TGGGTCCGGTTCTATGCCAACCTGTTACCGGAGGTGATCGATCTTACCTGCCACGAGG
----- Ela gene -----



FIGURE 3B

961 CTGGCTTCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTGTGTTAGATTATG
 -----Ela gene-----
 1021 TGGAGCACCCCGGGCACGGTGCAGGTCTTGTCTATTATCACCGGAGGAATACGGGGAC
 -----Ela gene-----
 1081 CAGATATTATGTGTTCGCTTIGCTATATGAGGACCTGTGGCATGTTGTCTACAGTAAGT
 -----Ela gene-----
 1141 GAAAATTATGGCAGTGGGTGATAGAGTGGTGGGTTGGTGTGGTAATTTTTTTAAAT
 -----Ela gene-----
 1201 TTTTACAGTTTGTTGGTTAAAGAATTGTATTGTGATTTTAAAGGTCTGTGTC
 -----Ela gene-----
 1261 TGAACTGAGCCTGAGCCCGAGCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCTAA
 -----Ela gene-----
 1321 AATGGCGCCTGCTATCCTGAGACGCCGACATCACCTGTGCTAGAGAATGCAATAGTAG
 -----Ela gene-----
 1381 TACGGATAGCTGTGACTCCGGTCTTCAACACACCTCCTGAGATAACCCGGTGGTCCC
 -----Ela gene-----
 1441 GCTGTGCCCATAAACCAGTTGCCGTGAGAGTTGGTGGCGTCGCCAGGCTGTGGAATG
 -----Ela gene-----
 1501 TATCGAGGACTTGCTTAACGAGCCTGGCAACCTTGGACTTGAGCTGTAAACGCCAG
 -----Ela gene-----
 1561 GCCATAAGGTGAAACCTGTGATTGCCGTGTTAACGCCCTTGTGGCTGAATGAGT
 -----Ela gene-----
 1621 TGATGTAAGTTAATAAAGGGTGAGATAATGTTAACCTGCTGGTAAATCTGACCTCATGG
 -----+-----
 1681 GGGGCTTAAAGGGTATATAATGCCCGTGGCTAACCTGGTACATCTGACCTCATGG
 -----Ela gene-----
 1741 GGCTTGGAGTGTGTTGGAAGATTTCTGCTGTGCGTAACCTGCTGGAACAGAGCTCAA
 -----Ela gene-----
 1801 CA
 --



FIGURE 3C

33881 AACCTACGCCAGAAAGCCAAAAACCCACAACCTCCTCAAATCGTCACTTCGGT
 33941 TTTCCCACGTTACGTACCTCCATTAAAGAATTCTACAATTCCAACACATACA
 34001 AGTTACTCCGCCCTAAAACCCGGCGAGTCTCCACGTAAACGGTCAAAGTCCCCGGC
 +-----packaging signal-----
 34061 CCTAGACAAATATTACGCGCTATGAGTAACACAAAATTATTCAGATTTCACTTCCTTA
 -----packaging signal-----
 34121 TTCAGTTCCCGCGAAATGGCCAAATCTTACTCGGTTACGCCAAATTACTACAAACA
 -----packaging signal-----
 34181 TCCGCCCTAAAACCGGGCGAAAATTGTCACTTCTGTGTACACGGGCCACACCAAAAACG
 +-----+
 34241 TCACTTTGCCACATCCGTCGCITACATGTGTTCCGCCACACTGCAACATCACACTTCC
 34301 GCCACACTACTACGTACCCGCCCGTTCCACGCCCGGCCACGTACAAACTCCACC
 +-----ITR-----+
 34361 CCCTCATTATCATATTGGCTCAATCCAAAATAAGGTATATTGATGATG
 -----ITR-----+



FIGURE 4

1 CATCATCAATAATACTTATTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----

61 TTGTGACGTGGCGCGGGCGTGGGACGGGGCGGGTGACGTAGGGCGGCCGTAGCGAT
-----ITR-----+---MCS-----

121 ATCGGATCCCGGTGACTGAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGA
-----+-----Ela-----

181 AGAAATGCCGCCAGTCTTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTCC
-----Ela-----

241 ACCCTCTAGCCATTGAAACCACCTACCCCTCACGAACCTGTATGATTTAGACGTGACGGC
-----Ela-----

301 CCCCGAAGATCCCAACGAGGAGGCGGTTTCGAGATTTTCCCGACTCTGTAATGTTGGC
-----Ela-----

361 GGTGCAGGAAGGGATTGACTTACTCACTTTCCGCCGGCGCCCGTTCTCCGAGGCC
-----Ela-----

421 TCACCTTCCGGCAGCCGAGCACCGGGAGCAGAGAGCCTGGTCCGGTTCTAGCC
-----Ela-----

481 AACACCTGTACCGGAGGTGATCGATCTTACCTGCCACGAGGCTGGCTTCCACCCAGTGA
-----Ela-----

541 CGACGAGGATGAAGAGGGTGAGGAGTTGTGTTAGATTATGTGGAGCACCCGGCACGG
-----Ela-----

601 TTGCAGGTCTTGTCAATTACCCGGAGGAATACGGGGACCCAGATATTATGTGTTCGCT
-----Ela-----



FIGURE 5

1 CATCATCAATAATACCTTATTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----+

61 TTGTGACGTGGCGCGGGCGTGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
+-----ITR-----+-----+-----

121 CGATACCGTCGAAACTTGTAACTGCAGCTTATAATGGTTACAATAAGCAATAGCATIC
-----polyA-----

181 ACAAAATTCACAAATAAGCATTTCACTGCATTCTAGTTGTGGTTGTCCAAACTC
-----polyA-----

241 ATCAATGTATCTTATCATGTCTGGATCCCGCGCCGCTAGCGATATCGGATCCCGGTGACT
-----+-----+-----

301 GAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCGCCAGTCT
-----Ela-----

361 TTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTGAA
-----Ela-----

421 ACCACCTACCCCTCACGAACTGTATGATTTAGACGTGACGGCCCCGAAGATCCAACGA
-----Ela-----

481 GGAGGCGGTTTCGAGATTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGAA
-----Ela-----

541 CTTACTCACTTTCCGCCGGCGCCCGGTTCTCCGAGCCGCCTCACCTTCCGGCAGCC
-----Ela-----

601 CGAGCAGCCGGAGCAGAGAGCCTGGGTCCGGTTCTATGCCAACCTGTACCGGAGGT
-----Ela-----



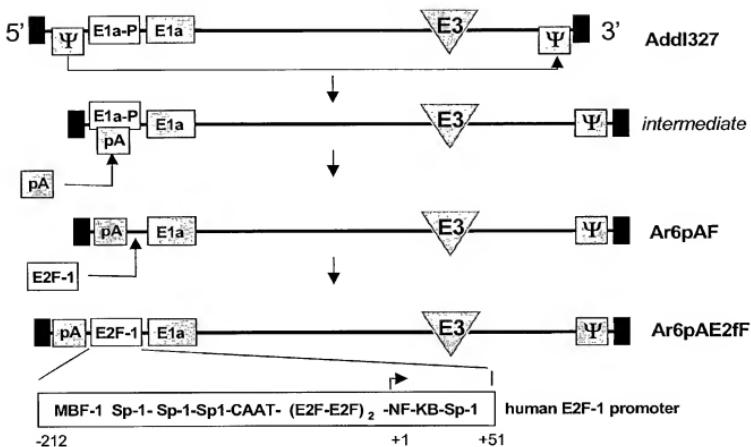


FIGURE 6



Fig. 7 Body weight change

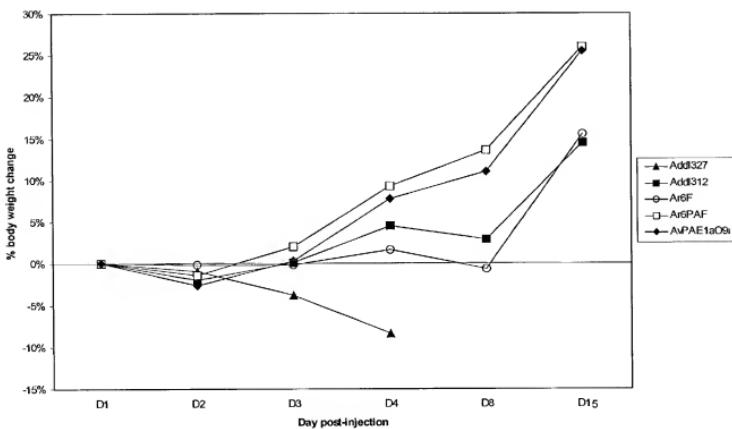


Fig. 8 Minimizing nonspecific transactivation of E1a gene

Backbones generated:

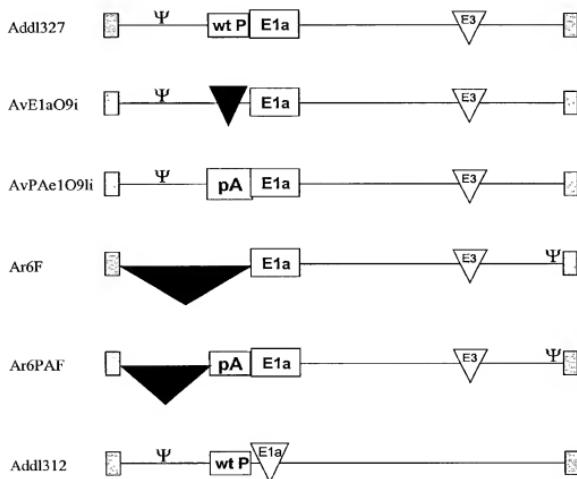


Figure 9. Mean H460 tumor volume

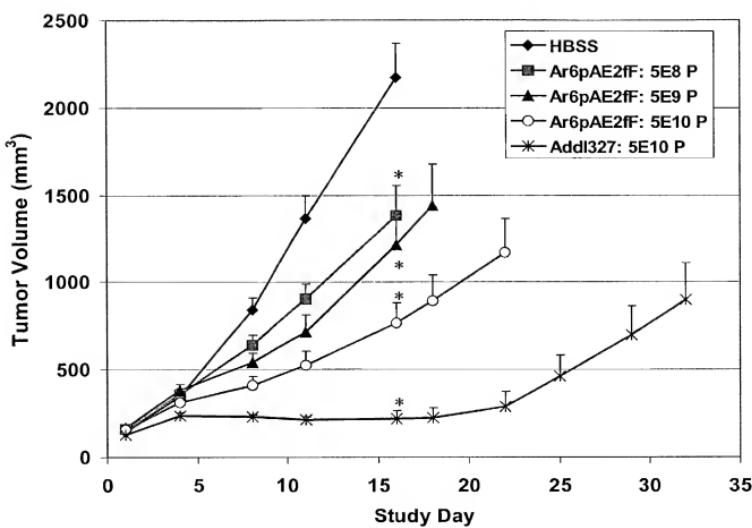


FIGURE 10

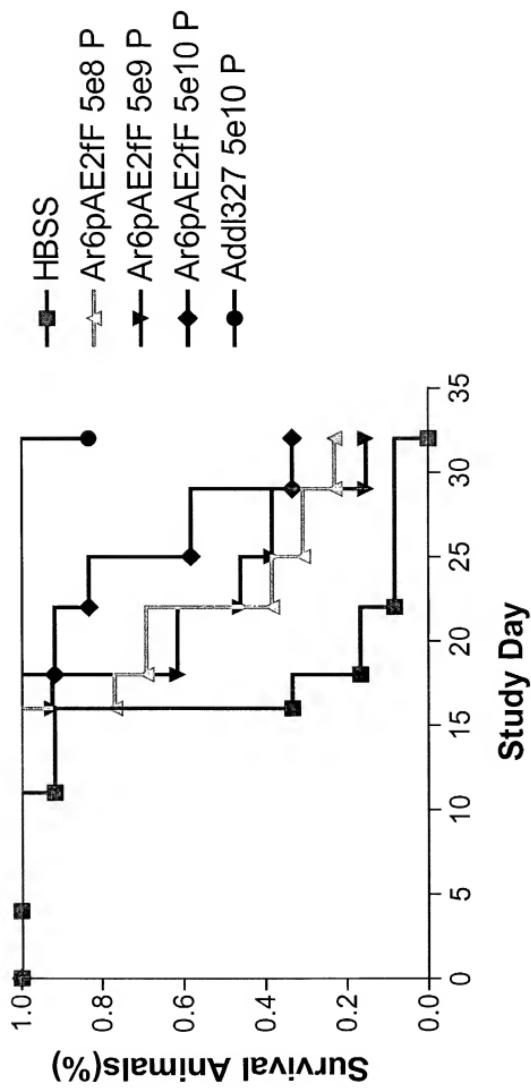


FIGURE 11

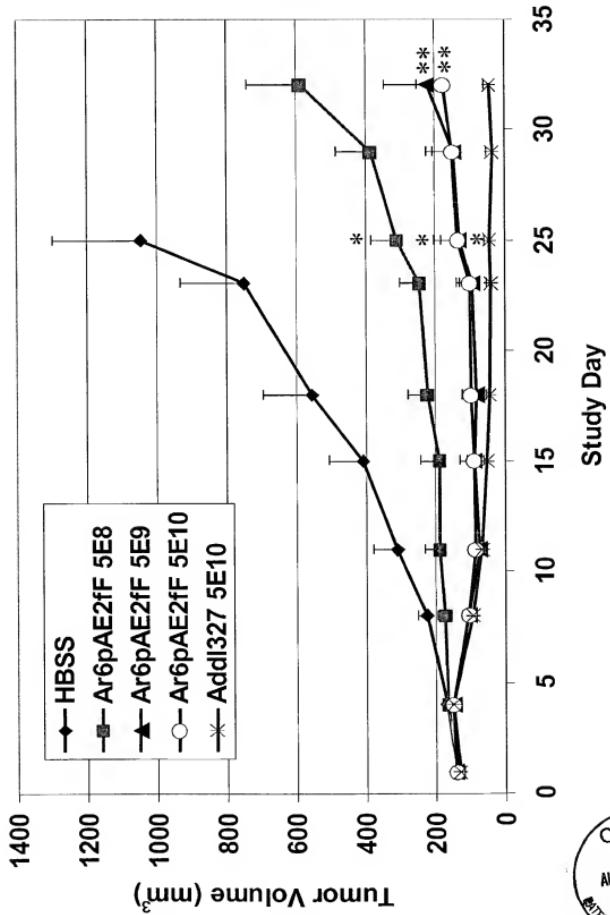
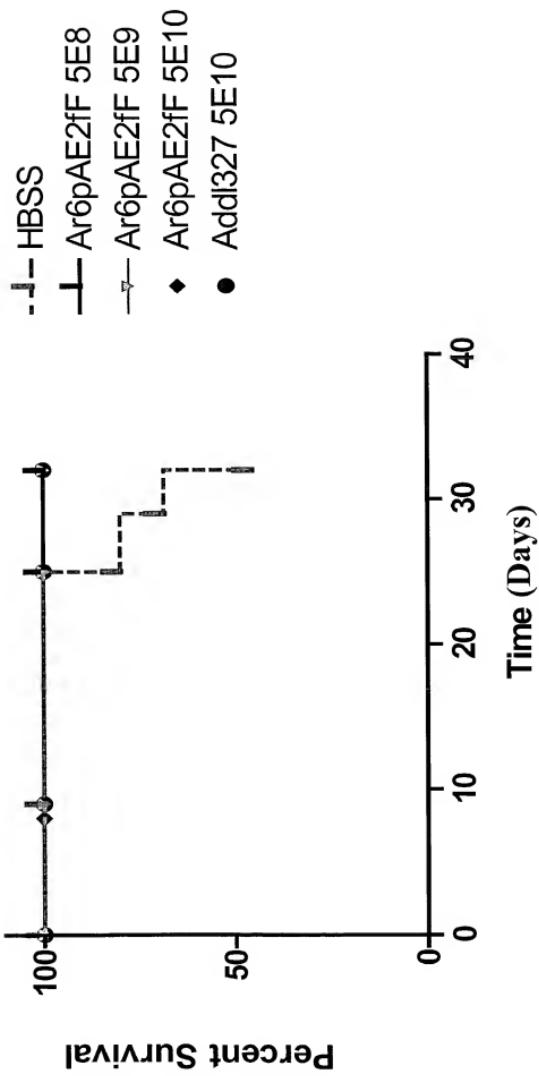


FIGURE 12



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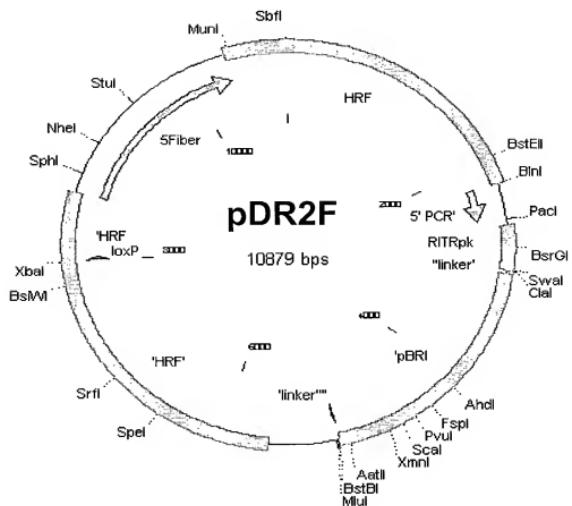
FIGURE 13

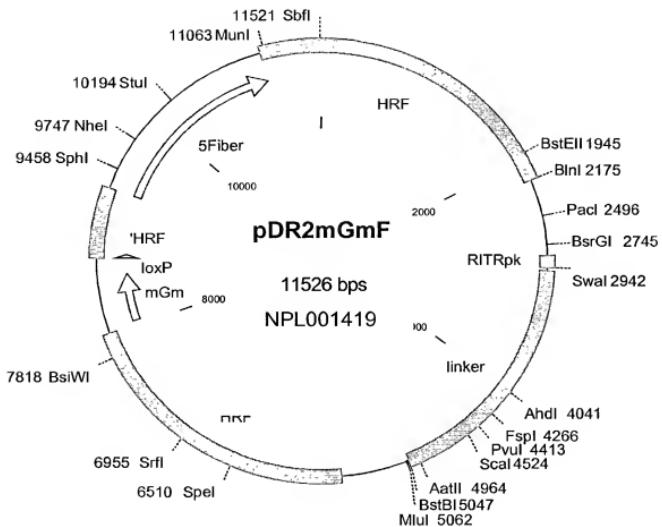
FIGURE 14

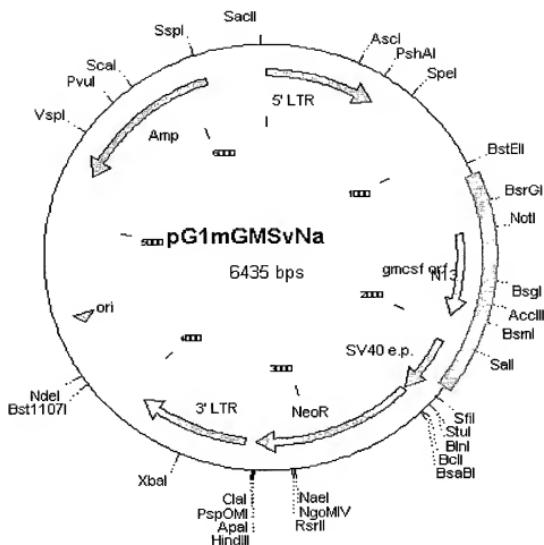
FIGURE 15

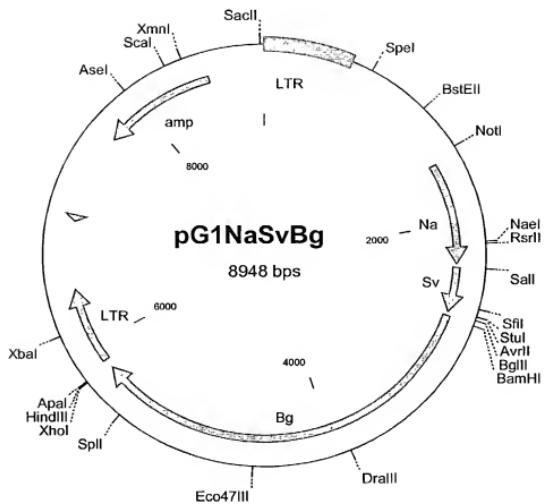
FIGURE 16

FIGURE 17

7878 TTCCGGACAG ACCTCAATAA CTCGTGTTAC CAGAACAGGA GGTGAGCTTA
7928 GAAAACCCCTT AGGGTATTAG GCCAAAGGGCG CAGCTACTGT GGGGTTTATG
7978 AACAACTCAA GCAACTCTAC GGGTATTCT AATTCAAGGTT TCTCTAGCCG
8028 GGCTGCAGGA ATTGATGGC CGCTACCTAC AATGGCCCAC GAGAGAAAGG
M A H E R K
8078 CTAAGGTCTT GAGGGAGATG TGCTGCAGA ATTTACTTTT CCTGGCATT
A K V L R R M W L Q N L L F L G I
8128 GTGGTCTACA GCCTCTCAGC ACCCACCCGC TCACCCATCA CTGTCACCCG
V V Y S L S A P T R S P I T V T
8178 GCCTGGAAG CATGTAGAGG CCATCAAAGA AGCCCTGAAC CTCCTGGATG
R P W K H V E A I K E A L N L L D
8228 ACATGCCCTGT CACATTGAAT GAAGAGGTAG AAGTCGTCTC TAACGAGTTC
D M P V T L N E E V E V V S S N E F
8278 TCCTCAAGA AGCTAACATG TGTCAGACCG CGCCTGAAGA TATTGAGCA
S F K K L T C V Q T R L K I F E
8328 GGGCTACCGG GCCAATTCA CCAAACCTAA GGGCGCCTTG AACATGACAG
Q G L R G N F T K L K G A L N M T
8378 CCAGCTACTA CCAGACATAC TGCCCCCAA CTCCGAAAC GGACTGTGAA
A S Y Y Q T Y C P P T P E T D C E
8428 ACACAAAGTTA CCACCTATGC GGATTCATA GACAGCCTTA AAACCTTCT
T Q V T T Y A D F I D S L K T F
8478 GACTGATATC CCCTTGAAAT GCAAAAAACC AGTCCAAAAA TGAGGAAGCC
L T D I P F E C K K P V Q K -
8528 CAGGCCAGCT CTGAATCCAG CTTCTCAGAC TGCTGCTTTTG TGCCCTGCGT
8578 AATGAGCCAG GAACTCGAA TTTCTGCTT AAAGGGACCA AGAGATGTGG
8628 CACAGGTAGT CGAATCAAGC TTATCGATAC CGTCGACCTC GACTAGATAA
8678 CTTCGTATAA TGTATGCTAT ACGAAGTTAT GCTAGAAATG GACGGAATTA
8728 TTACAGAGCA GCGCTGCTA GAAAGACGCA GGGCAGCGGC CGAGCAACAG
8778 CGCATGAATC AAGAGCTCCA AGACATGGTT AACTTGACCC AGTGCAAAA 8826



FIGURE 18

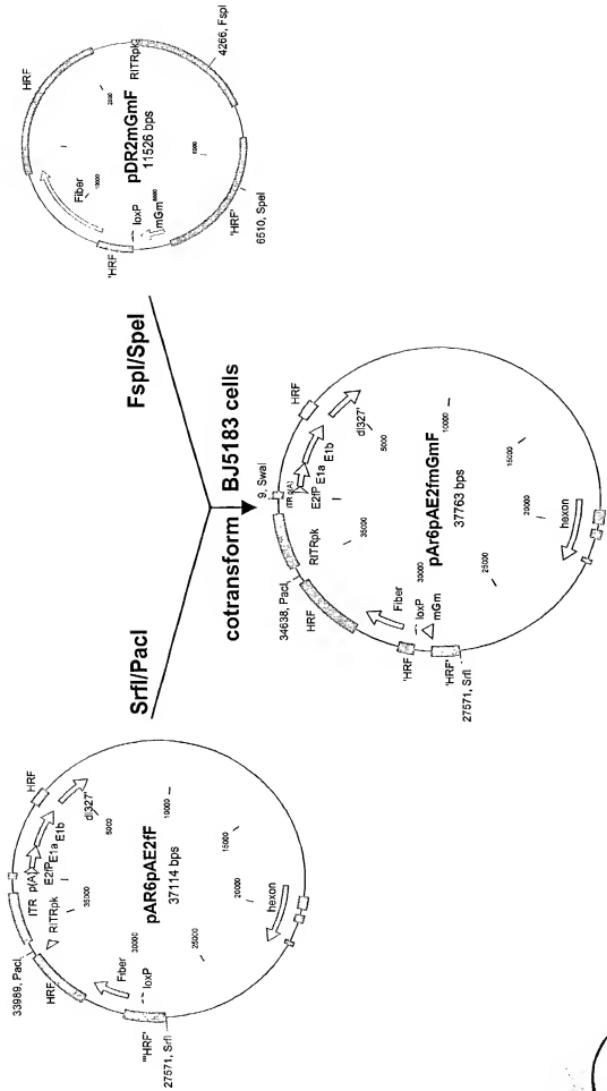
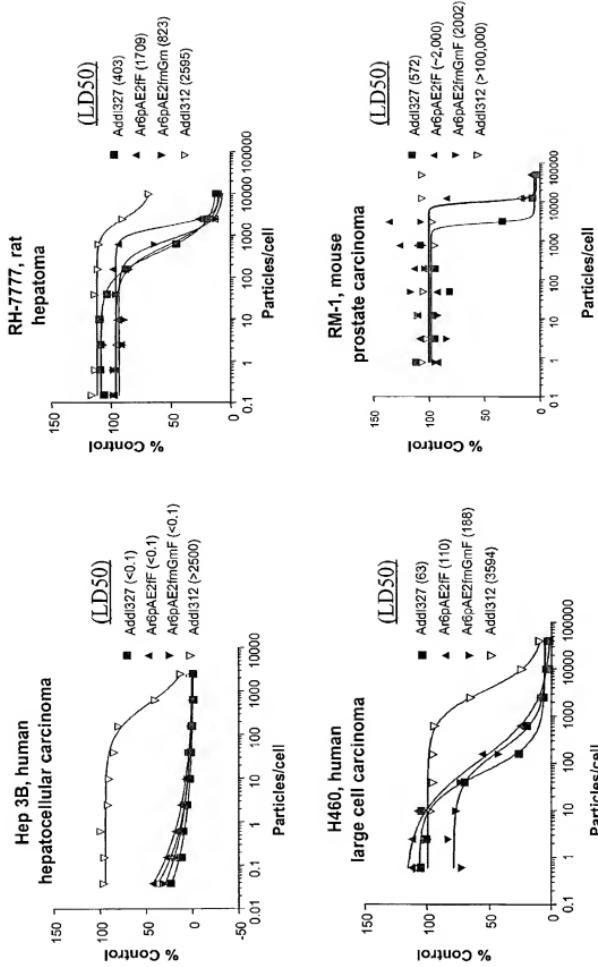


FIGURE 19



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FIGURE 20

28536 TATTAGGCCA AAGGCGCAGC TACTGTGGGG TTTATGAACA ATTCAAGCAA
 28586 CTCTACGGGC TATTCTAATT CAGGTTCTC TAGGATCTT CGCGCAGCAGC

 28636 CGCCACCATG TGGCTGCAGA GCCTGCTGCT CTTGGGCACT GTGGCTGCA
 M W L Q S L L L L G T V A C

 28686 GCATCTCTGC ACCCGCCCGC TCGCCCAGCC CCAGCACGCA GCCCTGGGAG
 S I S A P A R S P S P S T Q P W E

 28736 CATGTGAATG CCATCCAGGA GGCCCGGCGT CTCTGAACC TGAGTAGAGA
 H V N A I Q E A R R L L N L S R

 28786 CACTGCTGCT GAGATGAATG AAACAGTAGA AGTCATCTCA GAAATGTTTG
 D T A A E M N E T V E V I S E M F

 28836 ACCTCCAGGA GCGCACCTGC CTACAGACCC GCCTGGAGCT GTACAAGCAG
 D L Q E P T C L Q T R L E L Y K Q

 28886 GGCTGCGGG GCAGCCTCAC CAAGCTCAAG GGCCCCTTGA CCATGATGGC
 G L R G S L T K L K G P L T M M

 28936 CAGCCACTAC AAGCAGCACT GCCCCTCAAAC CCCGGAAACT TCCTGTGCAA
 A S H Y K Q H C P P T P E T S C A

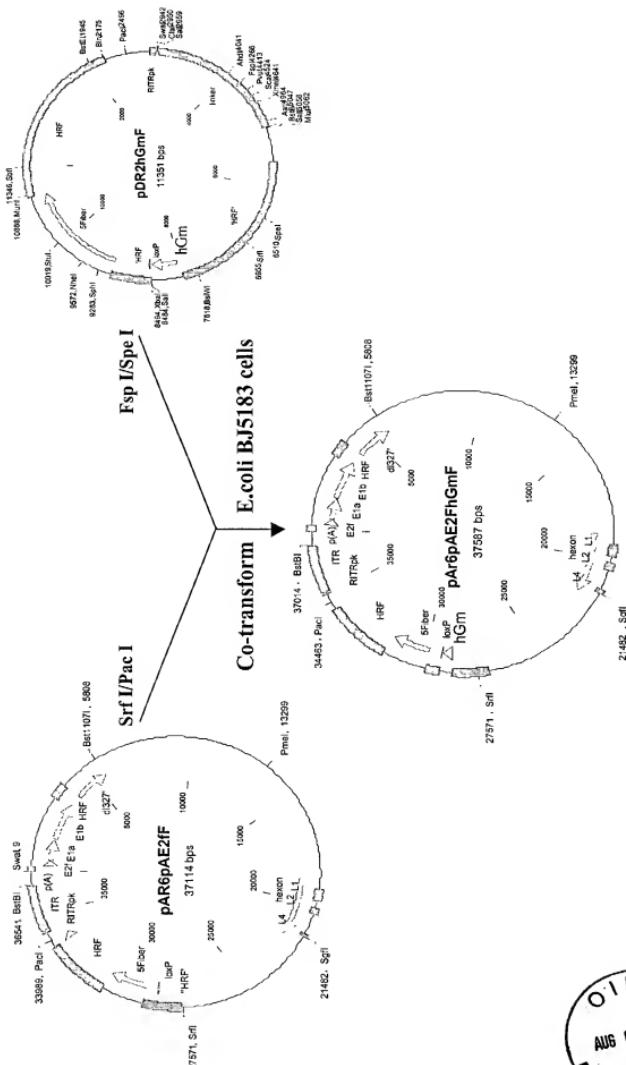
 28986 CCCAGACTAT CACCTTTGAA AGTTTCAAAG AGAACCTGAA GGACTTTCTG
 T Q T I T F E S F K E N L K D F L

 29036 CTTGTCATCC CCTTTGACTG CTGGGAGCCA GTCCAGGAGT GAGTCGACAA
 L V I P F D C W E P V Q E -

 29086 GCTCTAGATA ACTTCGTATA ATGTATGCTA TACGAAGTTA TGCTAGAAAAT
 29136 GGACGGAATT ATTACAGAGC AGCGCTGCT AGAAAGACGC AGGGCAGCG
 29186 CCGAGCAACA GCGCATGAAT CAAGAGCTCC AAGACATGGT TAACITGCAC
 29236 CAGTGCAAA GGGGTATCTT TTGTCTGGTA AAGCAGG 29273



FIGURE 21



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FIGURE 22

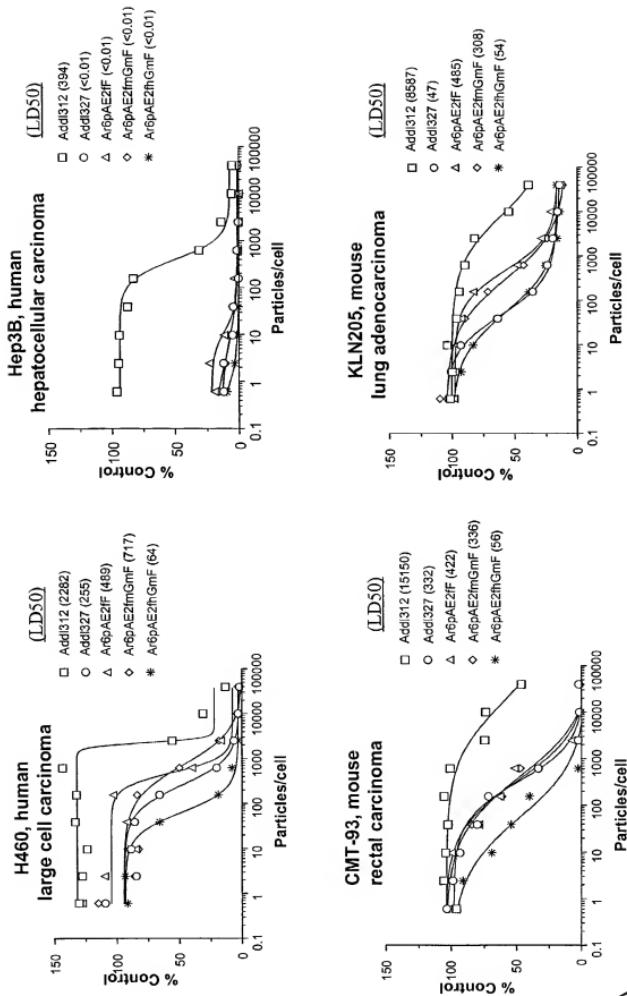


FIGURE 23

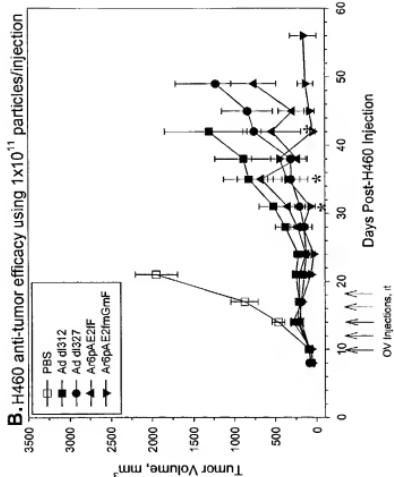
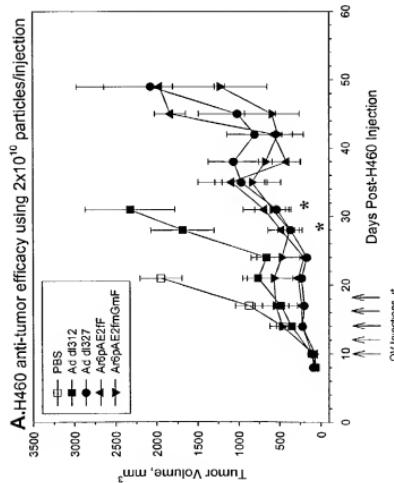


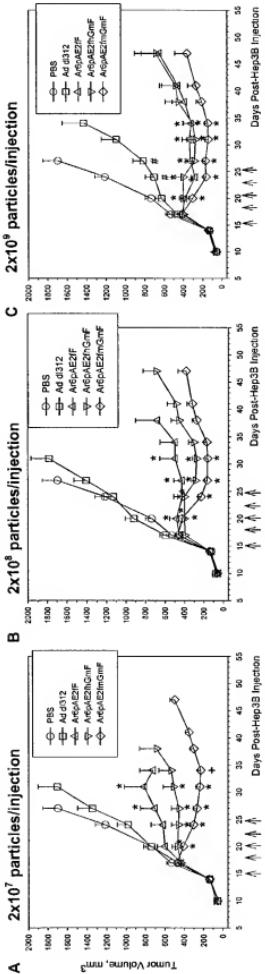
FIGURE 24

FIGURE 25

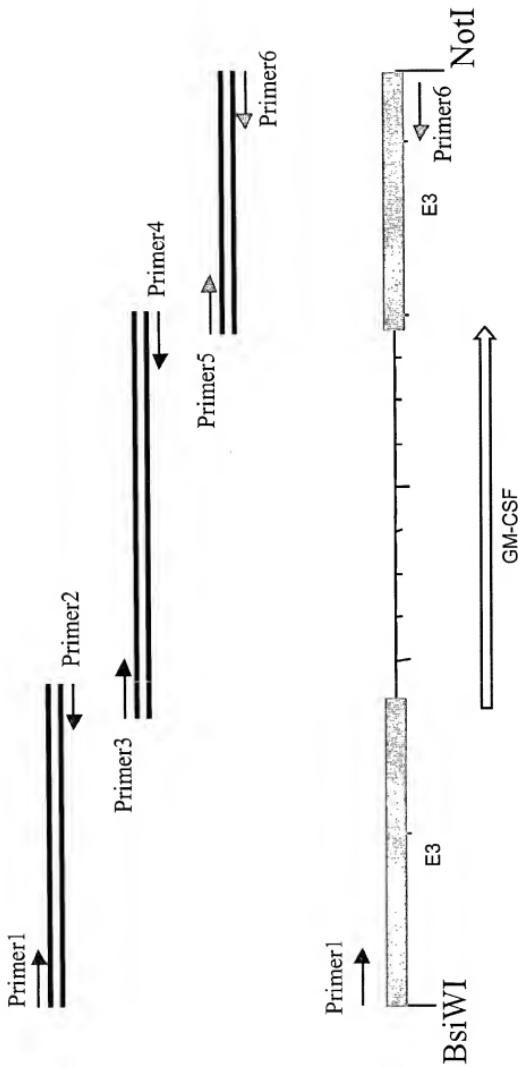


FIGURE 26A

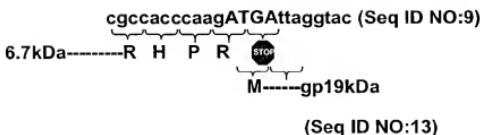


FIGURE 26B

1. Δgp19a: atgg
6.7kDa—plus 9aa to STOP M—mouse GMCSF

atgt
6.7kDa—plus 33aa to STOP M—human GMCSF

2. Δgp19b: cgcccaccaag ATAAACCATg..... (SEQ ID NO:98)
6.7kDa—R H P R STOP M—GMCSF

3. Δgp19c: cgcccaccaagatgA.....(Seq ID NO:10)
6.7kDa—R H P R STOP M—GMCSF

4. Δgp19d: cgcccaccaagATGAACCtg.....(Seq ID NO:11)
6.7kDa—R H P R STOP M T M—GMCSF

5. Δgp19b/IRES: cgcccaccaagatgCAATT...IRES...atg..... (Seq ID NO:12)
6.7kDa—R H P R STOP M—GMCSF



FIGURE 27A

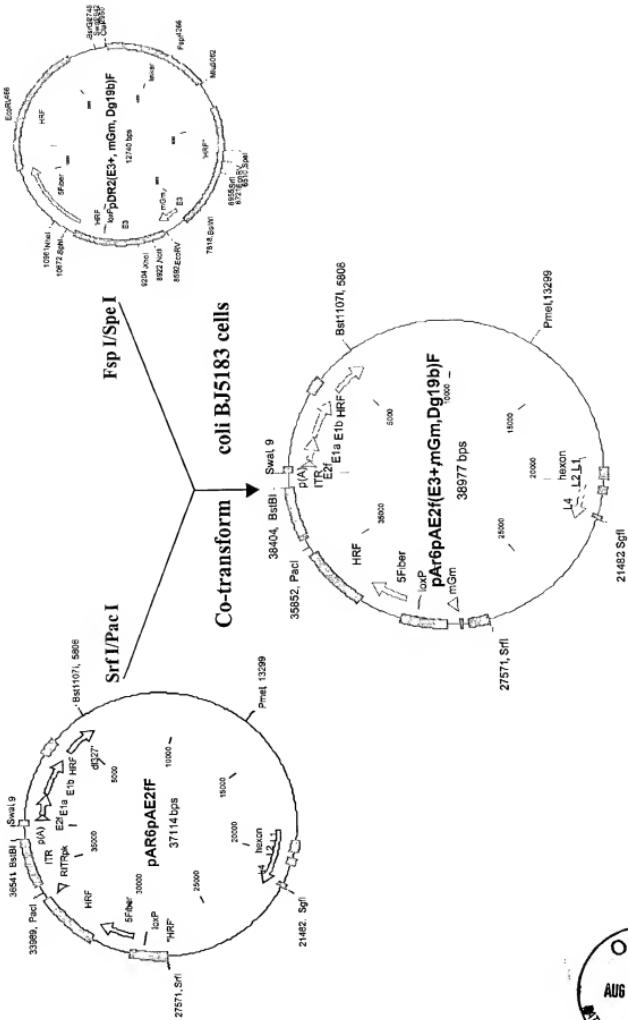
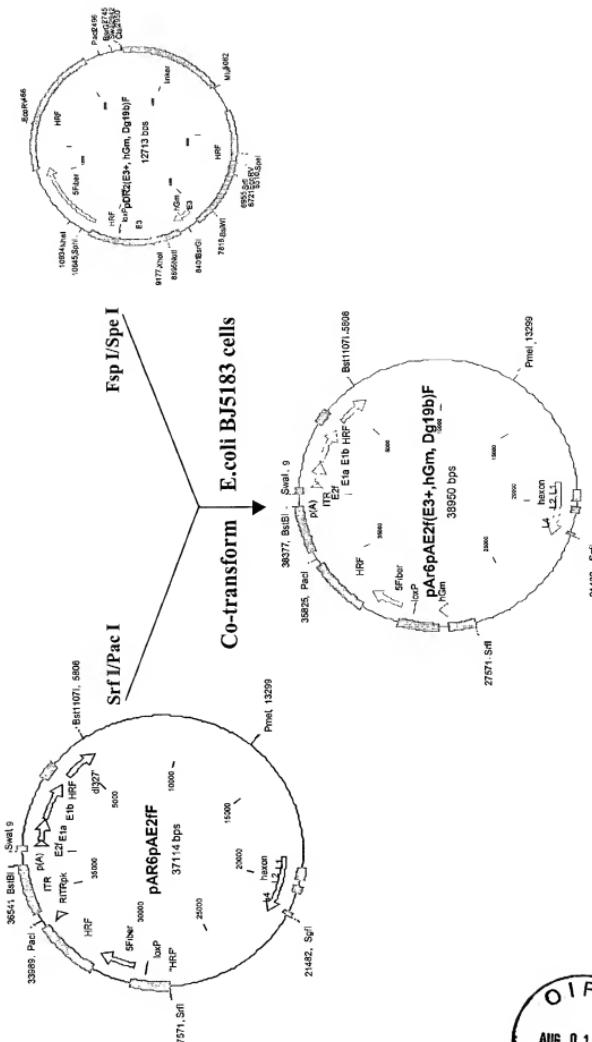


FIGURE 27B



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FIGURE 28

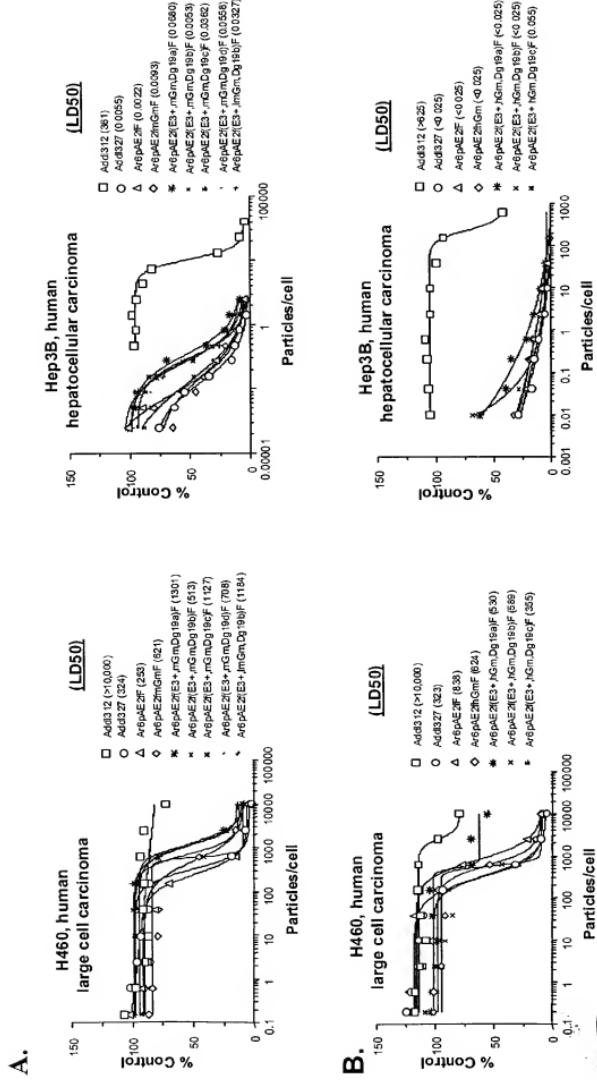


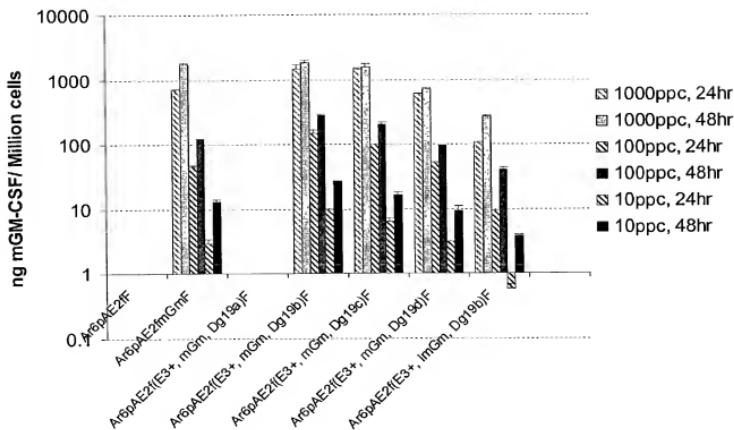
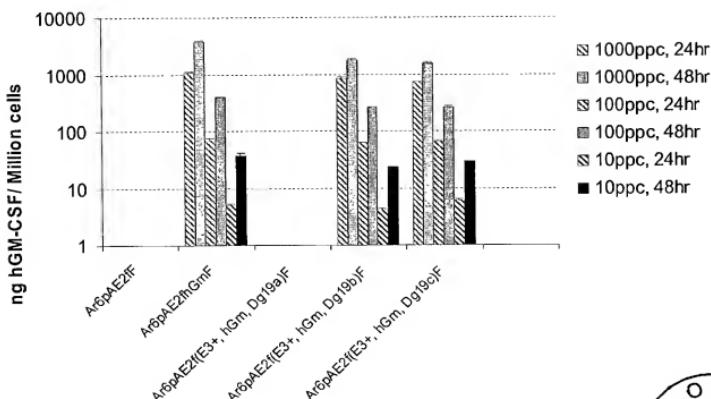
Figure 29**a. Mouse GM-CSF expression in H460 cells****b. Human GM-CSF expression in H460 cells**

Figure 30

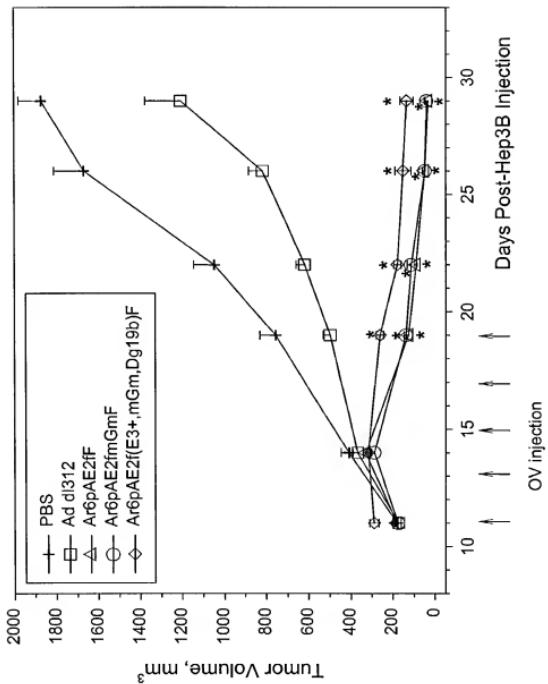




Figure 31

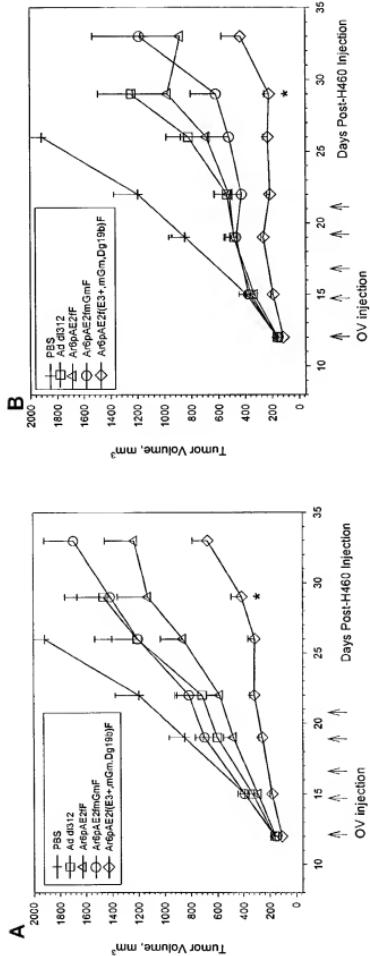


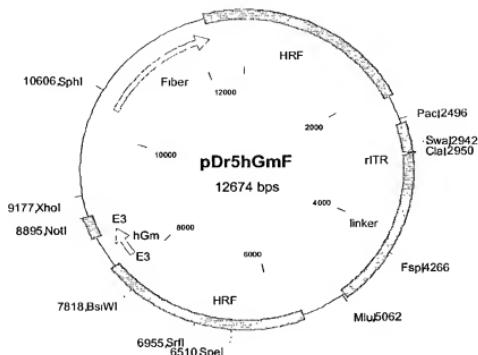
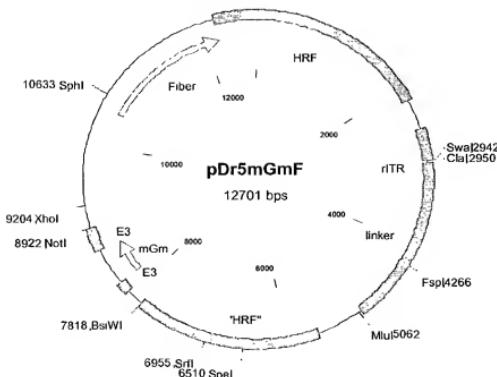
Figure 32**A. pDr5hGmF****B. pDr5mGmF**

Figure 33

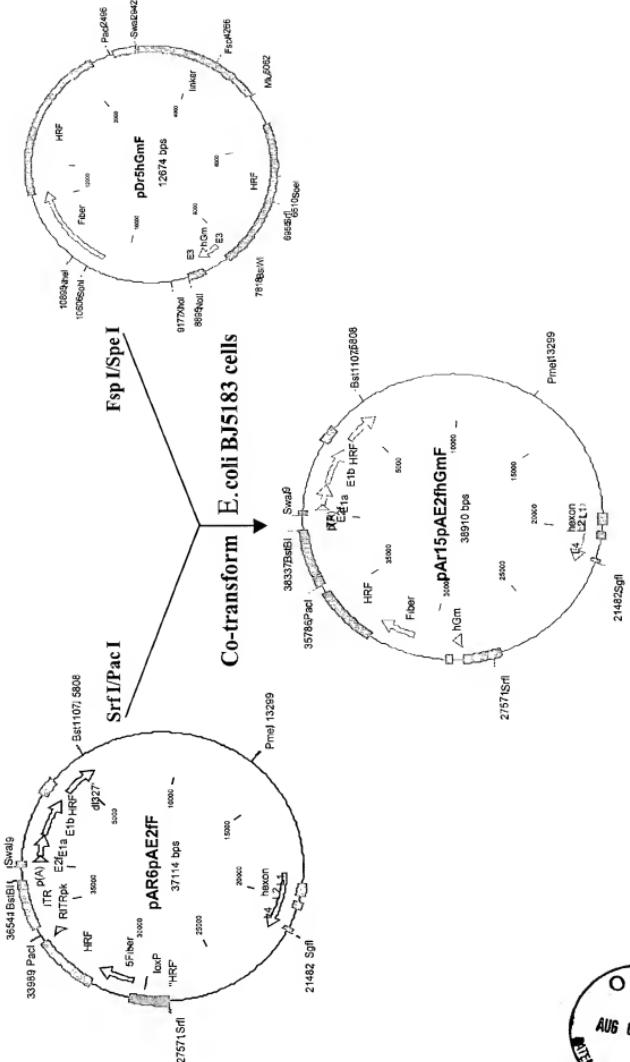


Figure 34

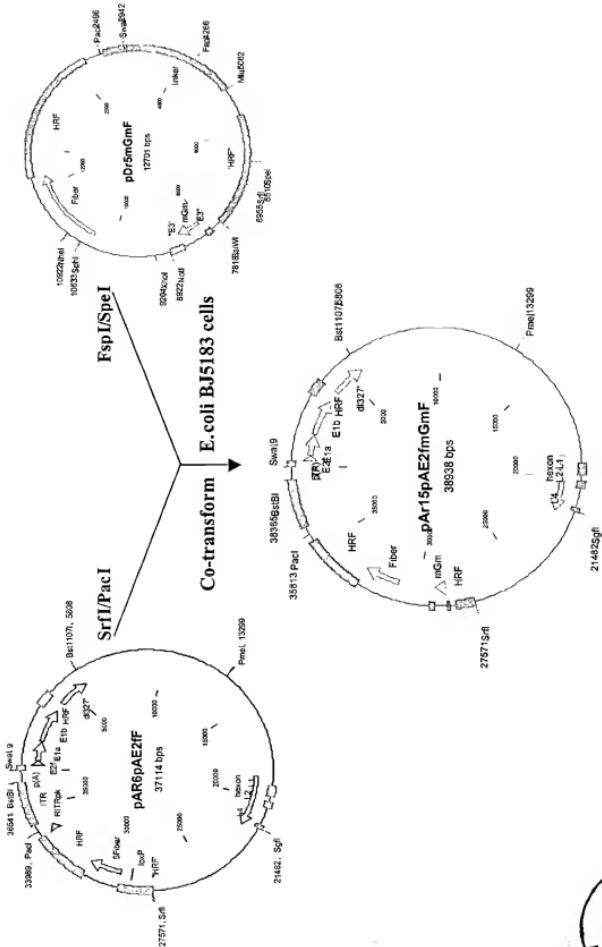


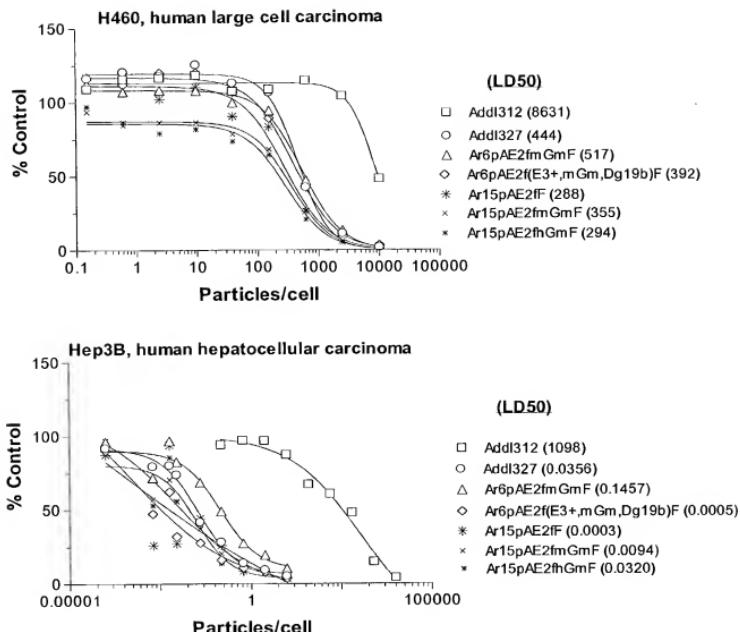
Figure 35

Figure 36

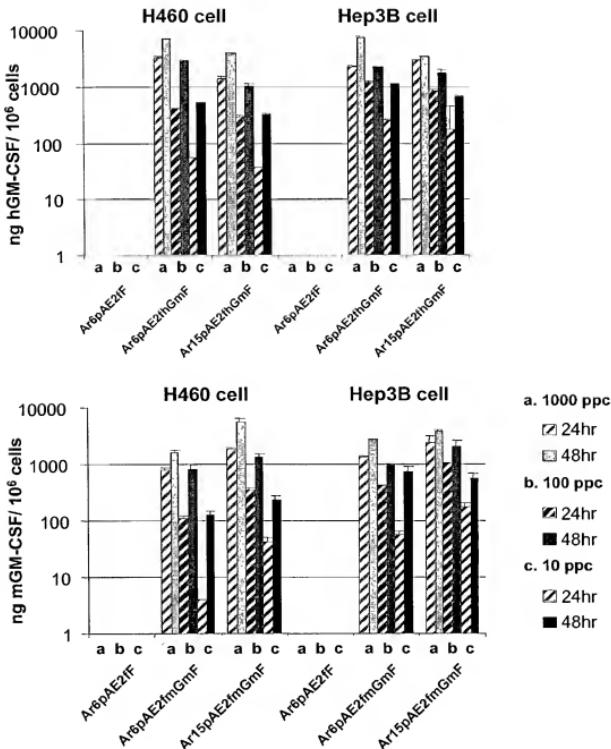


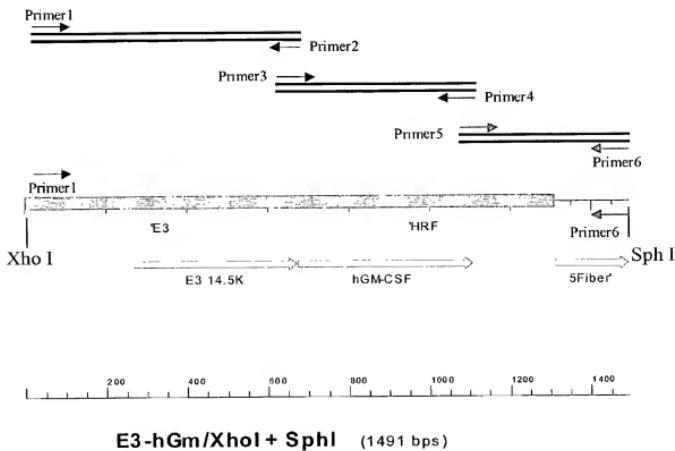
Figure 37

Figure 38A

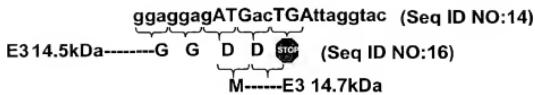


Figure 38B



Figure 39

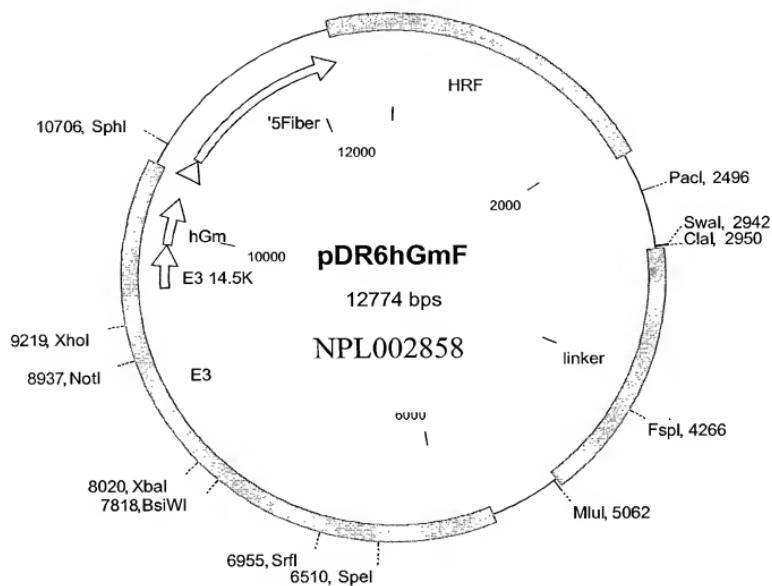


Figure 40

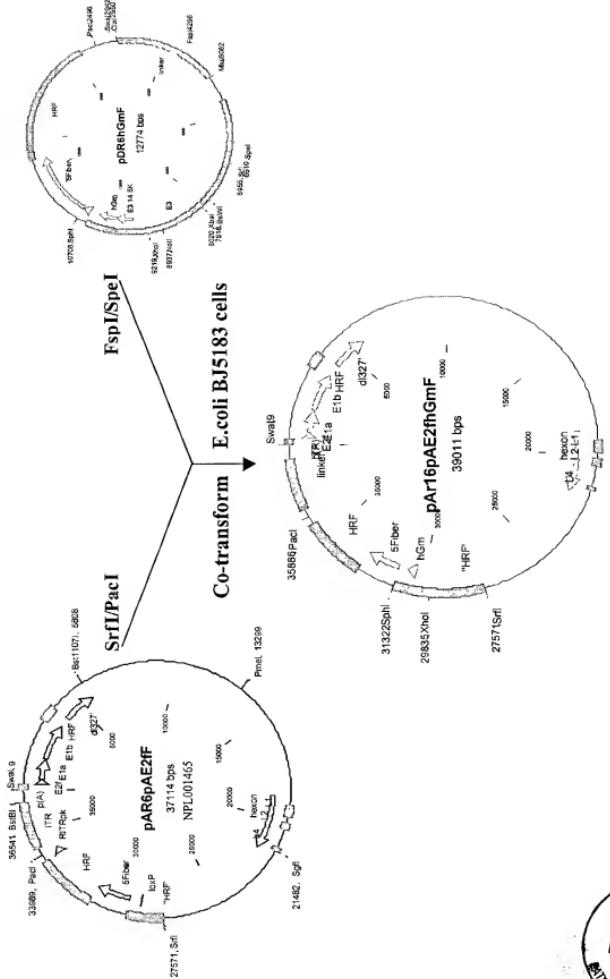


Figure 41

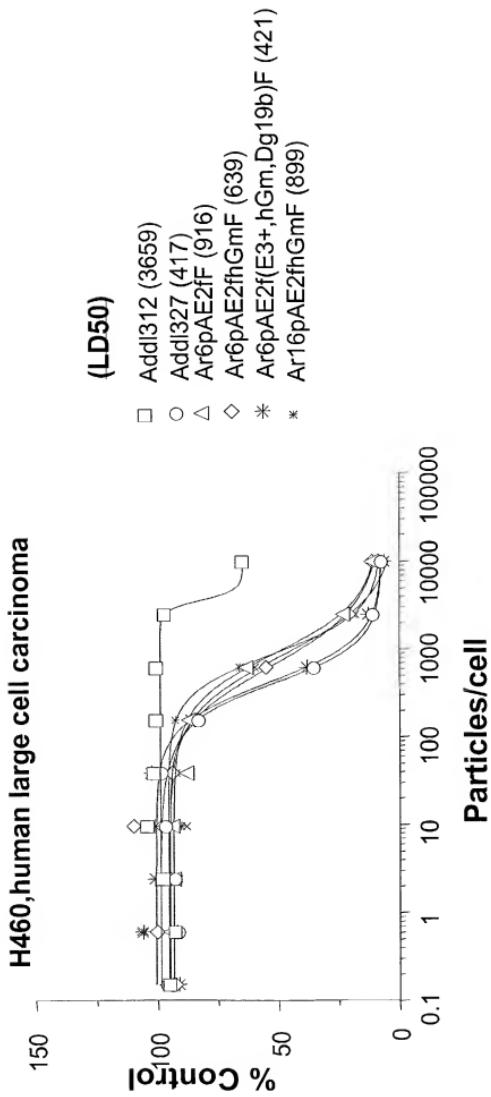


Figure 42

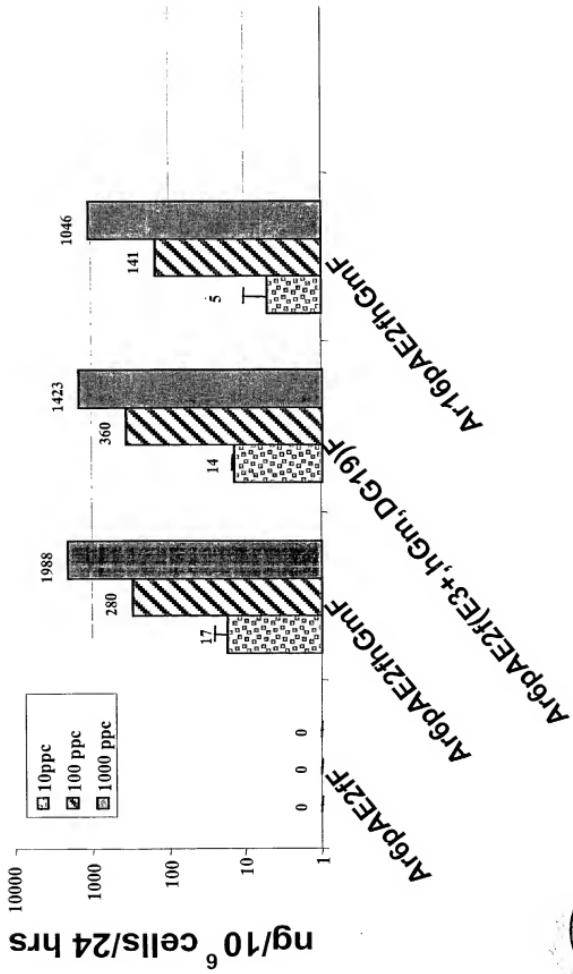
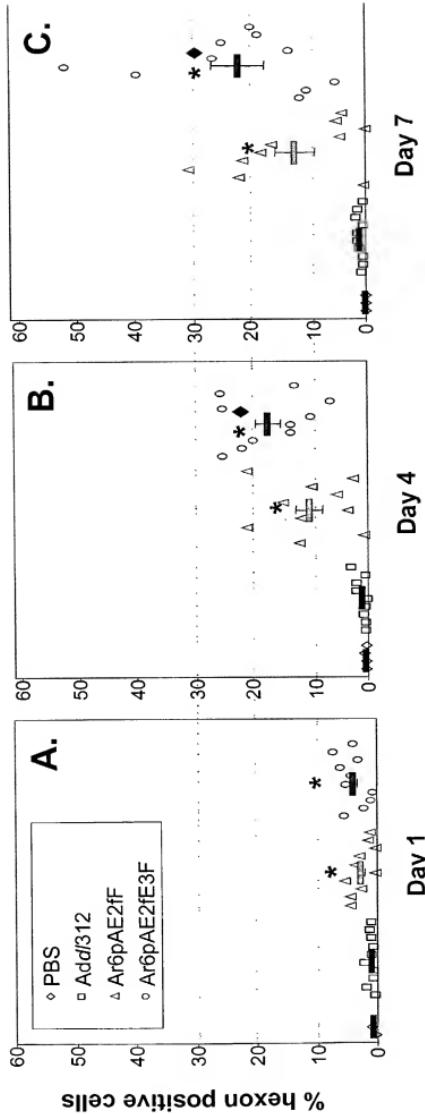


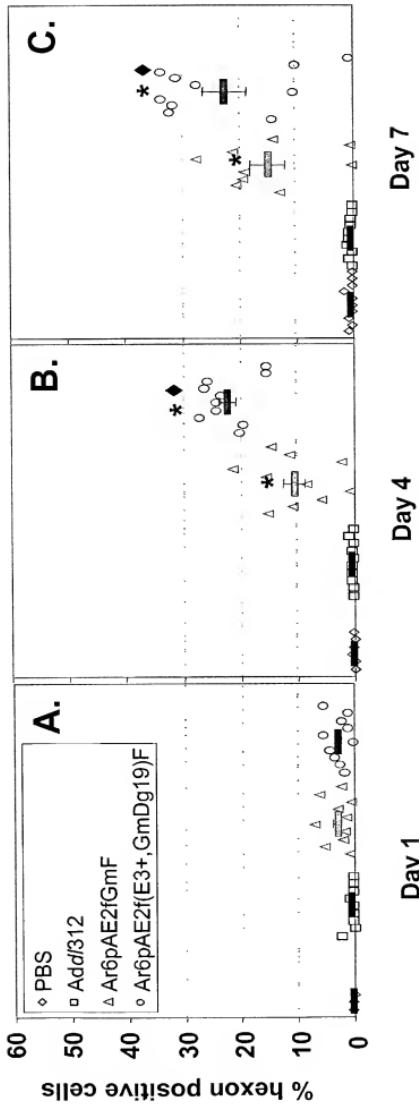
Figure 43



* p<0.05 between A6pAE2ff or A6pAE2fE3F and Add312, ANOVA
• p<0.05 between A6pAE2ff and A6pAE2fE3F vectors, ANOVA



Figure 44



*: p<0.05 between Ar6pAE2fGmF or Ar6pAE2f(E3+, hGm.Dg19)F and Add312, ANOVA
 -: p<0.05 between Ar6pAE2fGmF and Ar6pAE2f(E3+, hGm.Dg19)F vectors, ANOVA



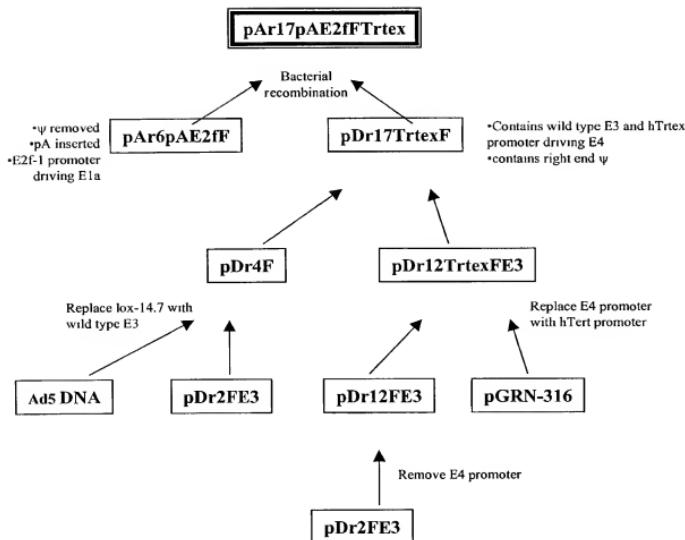
Figure 45

Figure 46

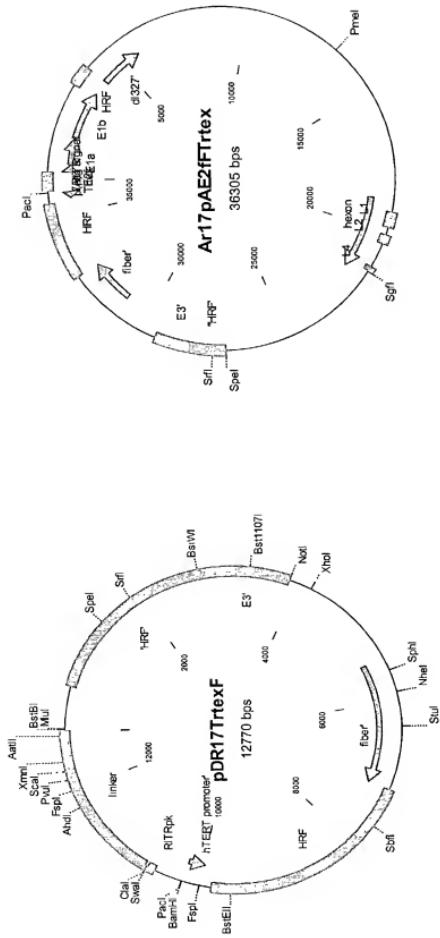


Figure 47

35351 agtgcataaa agcgaccgaa atagcccggg ggaatacata cccgcaggcg
35401 tagagacaac attacagccc ccataaggagg tataacaaaaa ttaataggag
35451 agaaaaaacac ataaaacccct cctgccttagg caaaaatagac
35501 ccctcccgct ccagaacaac atacagcgt tcacagcggc agctacaacg
35551 tcagccttac cagtaaaaaa gaaaacctat taaaaaaaaa ccactcgat
35601 caattcgcgg gggtggccgg ggcgcagggt tccccacgtgc gcagcaggac
35651 gcagcgcgtc ctgaaaactcg cgccgcggg agagggcggg qccgcggaaa
35701 ggaaggggag gggctggag ggccggagg gggctggcc ggggacccgg
35751 gaggggtcgg gacggggccgg ggtccgcgcg gaggaggcgg agctggaaagg
35801 tgaaggggca gacgggtgc cgggtccccc agtcctccg ccacgtgggg
35851 cttagatcct taattaagaa ttctacaatt ccaacacat acaagttact
35901 ccgcctaaa accctggggc agtctccacg taaacggtca aagtcccccc
35951 ggcccttagac aaatattacg cgctatgagt aacacaaaaat tattcagatt
36001 tcacttcctc ttattcgtt ttccgcgaa aatggccaaa tcttactcg
36051 ttacgccccaa atttactaca acatccgcct aaaacgcgcg gaaaattgtc
36101 acttcctgt tacaccggcg cacacaaaaa acgtcactt tgccacatcc
36151 gtcgcttaca tgtgtccgc cacacttgca acatcacact tccgccacac
36201 tactacgtca cccgccccgt tcccacggcc cgcgcacacgt cacaactcc
36251 accccctcat tatacatattg gttcaatcc aaaataaggt atattattga
36301 tgatg



Figure 48

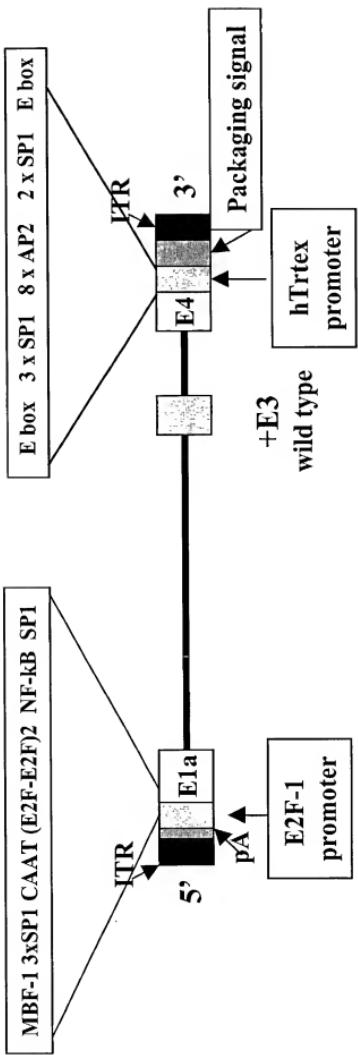


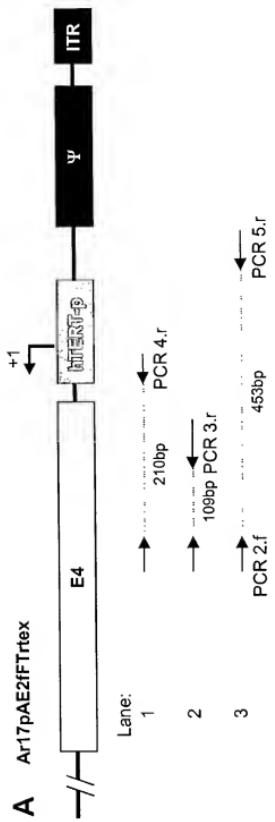
Figure 49

Figure 50

35521 ATACACGGCT TCAAGCGGCG AGCCAAACAG TGAGCCCTTAC CAGTAAAAAA GAAAACCTAT
ExtP1 ←
35581 TAAAAAAACA CAACTCGGAT CAATTCGCG GGGTGCCCG GGCCAGGGCT TCCCACGTGC
←
35641 GGACCGGAC GCAGGCCCTGC CTGAAACTCG CGCCCGCAGGG AGAGGGGG GCCCGGGAA
←
35701 AGCAAGGGA CGGGCTGGAA TGCCCCGGAA GGGGTGGGC CGGGACCG CGAGGGTC
35761 GGACCGGGC GGGGTCCGC CGGGCGAGG CGGACTCTGA AGGTGAAGG CGAGGACGG
35821 TGCCCGGGTC CCCAGTCCCT CGCCGACGTT CGGCTAGGAT CCTTAATTA GAATTCTACA
35881 ATCCCCAAC AATAAAGTT ACTCCGGCCCT AAAACCCTGG GCG



Figure 51

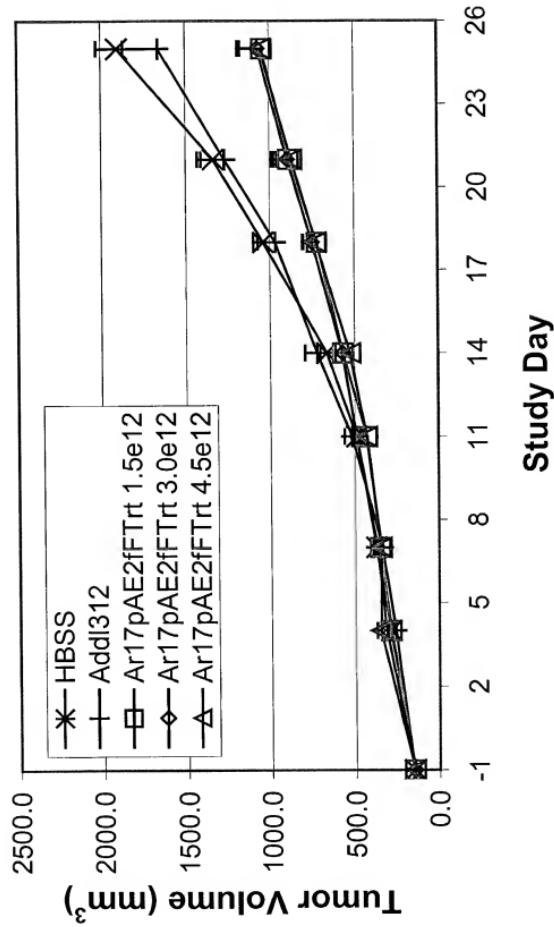


Figure 52

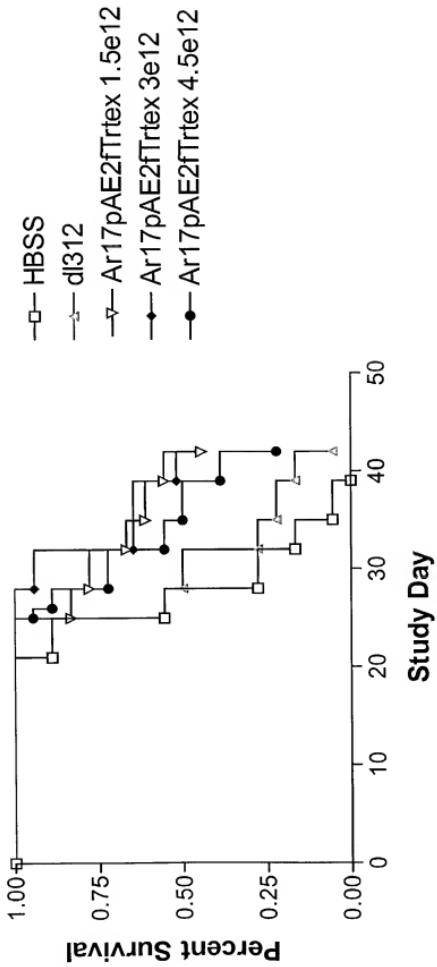


Figure 53

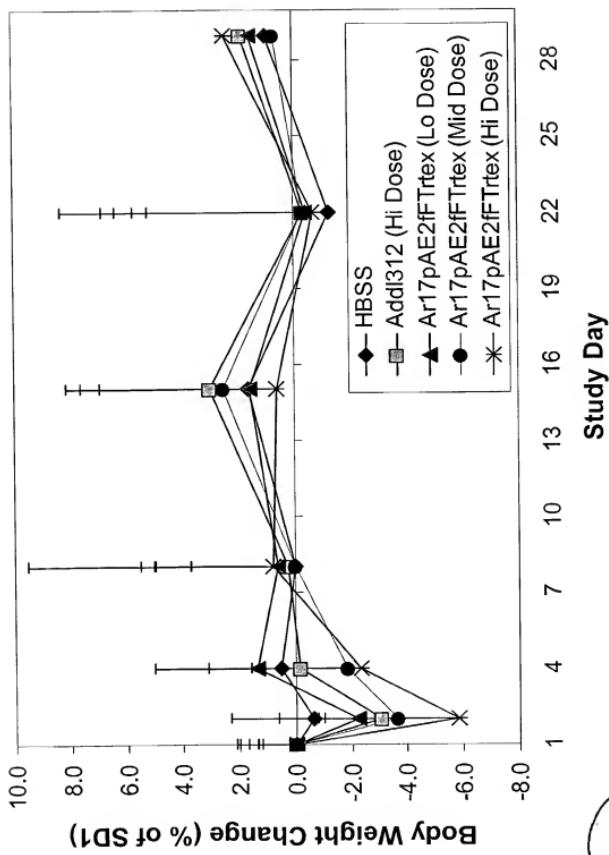


Figure 54

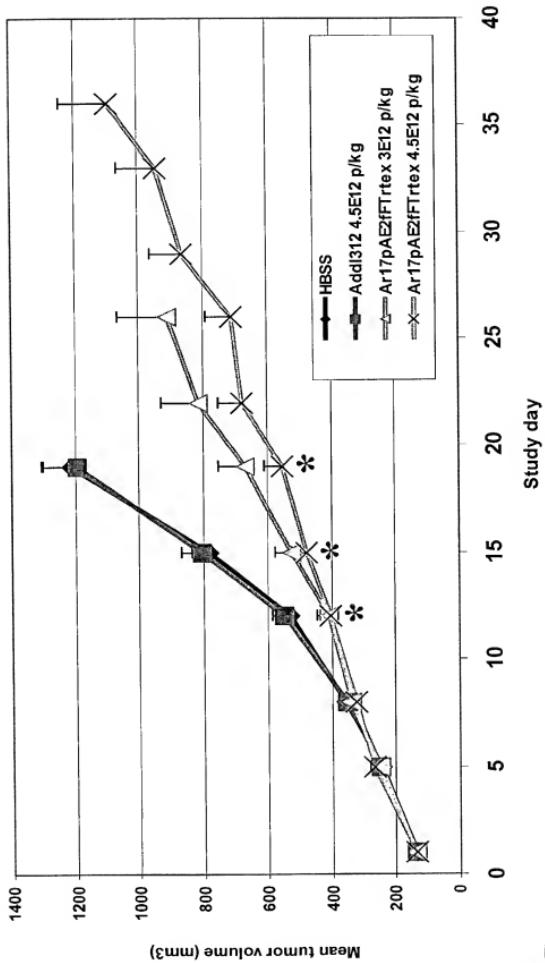


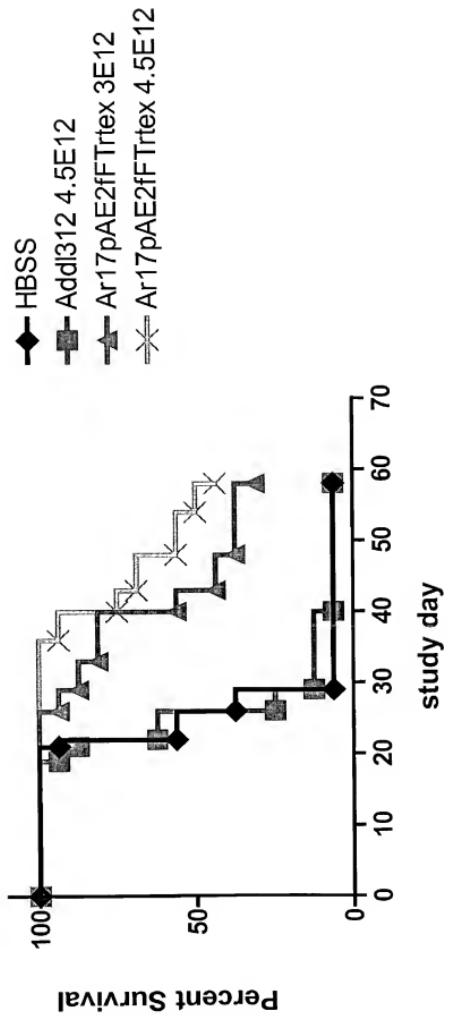
Figure 55

Figure 56

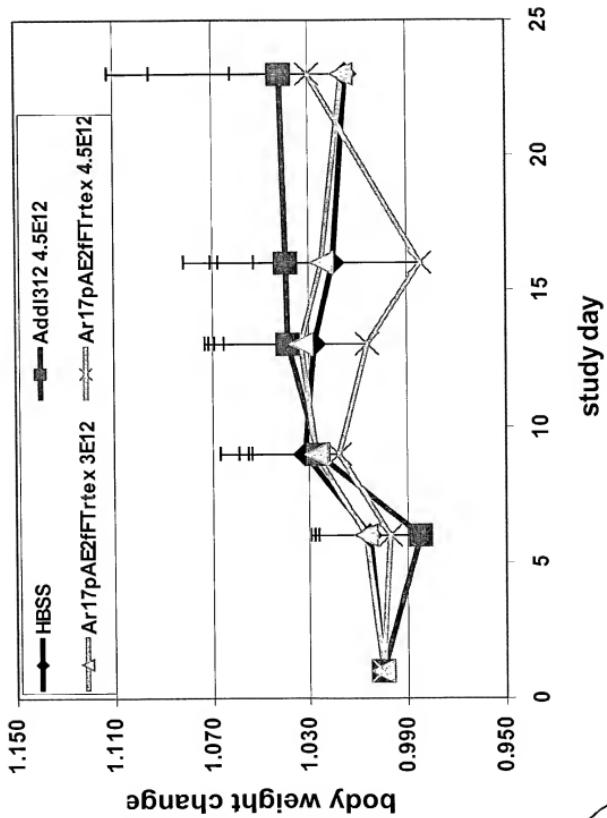


Figure 57

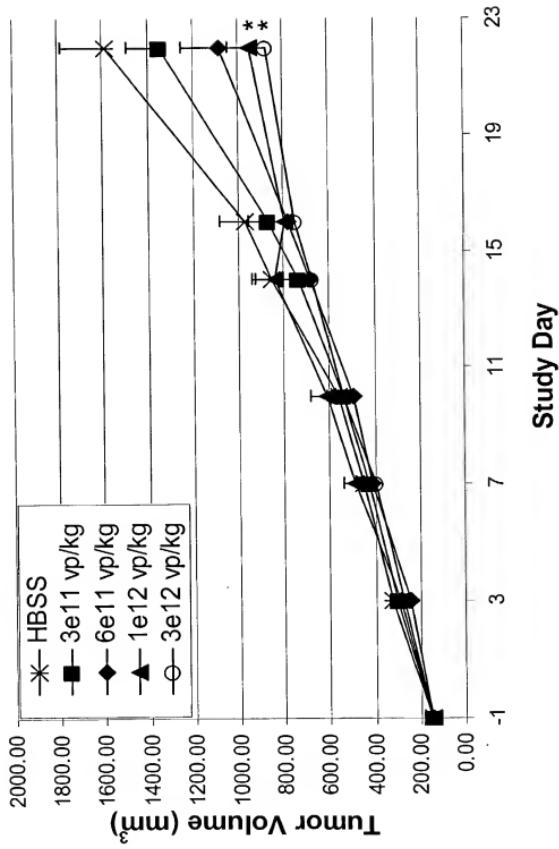


Figure 58

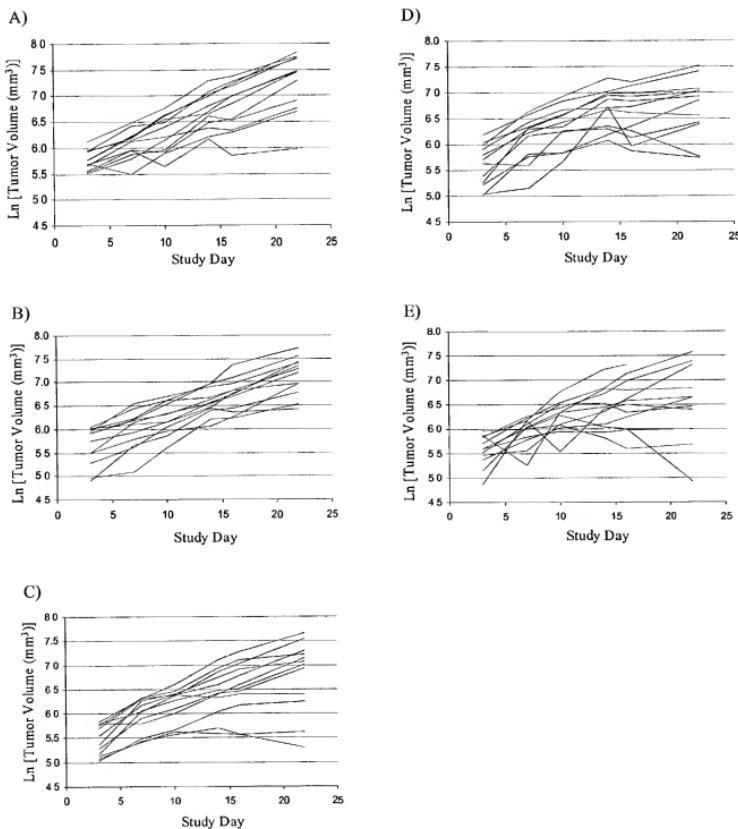


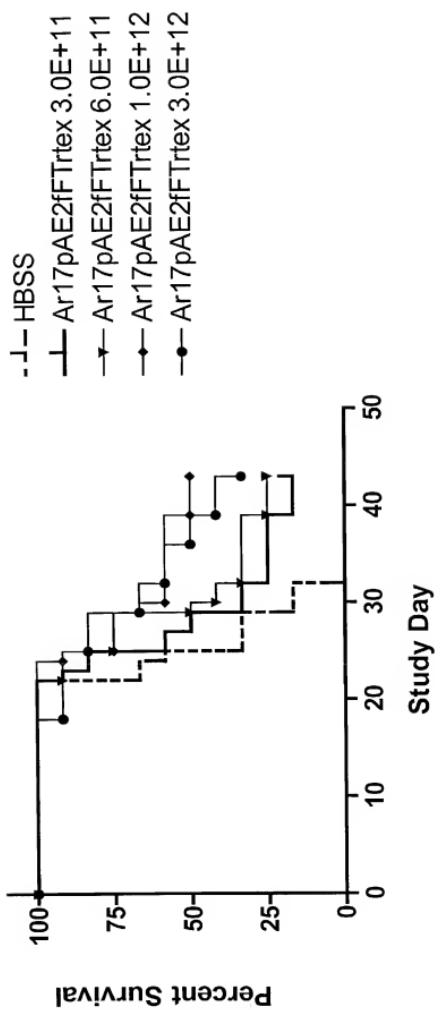
Figure 59

Figure 60

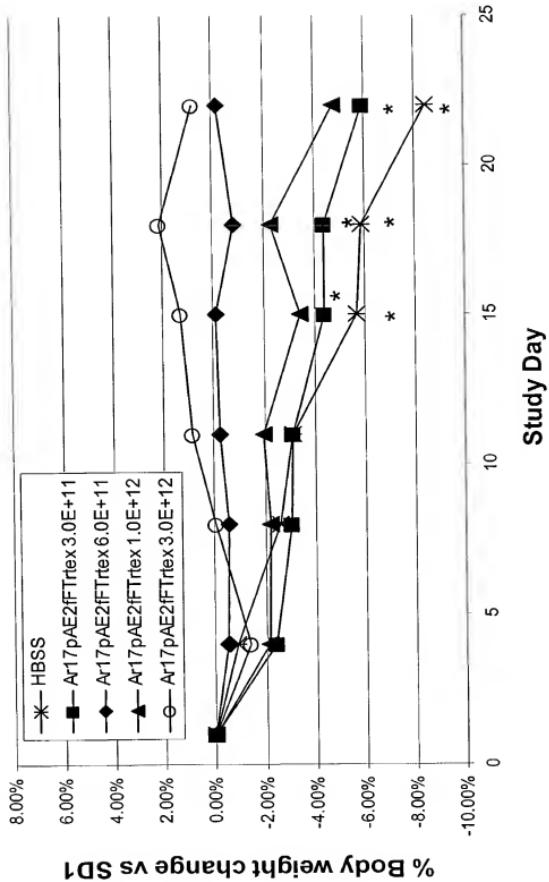


Figure 61

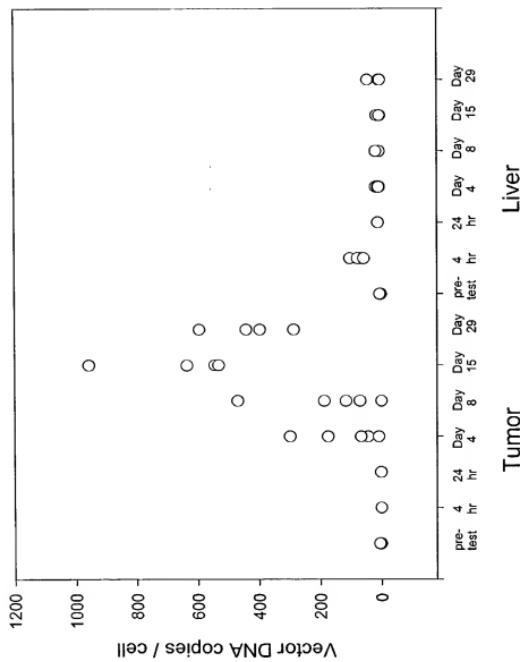
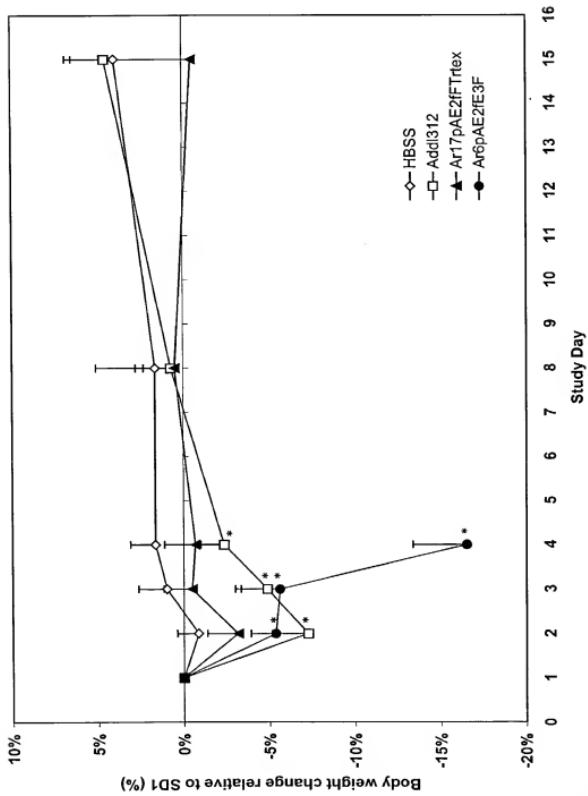
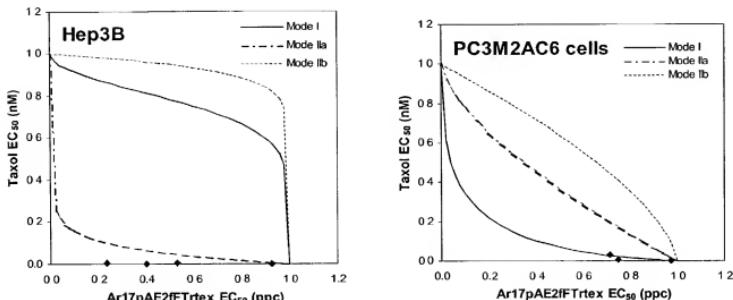


Figure 62

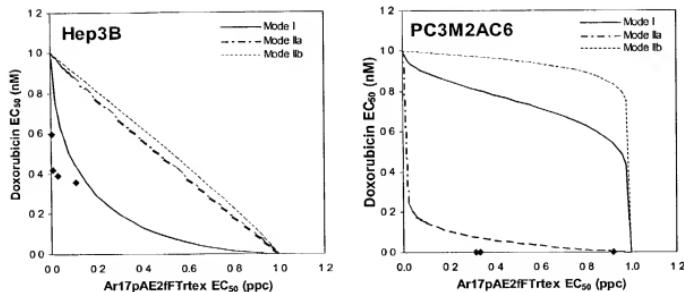
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1995

FIGURE 63

| MR (ppc/nM) | Virus EC ₅₀ ^b | Chemo EC ₅₀ ^b | Effect |
|-------------|-------------------------------------|-------------------------------------|---------|
| Virus alone | 1 | 0 | - |
| Chemo alone | 0 | 1 | - |
| 8.3e-05 | 0.23 | 0.0043 | synergy |
| 3.3e-04 | 0.53 | 0.0024 | synergy |
| 1.3e-03 | 0.40 | 0.00046 | synergy |
| 5.3e-03 | 0.93 | 0.00027 | synergy |

| MR (ppc/nM) | Virus EC ₅₀ ^b | Chemo EC ₅₀ ^b | Effect |
|-------------|-------------------------------------|-------------------------------------|------------|
| Virus alone | 1 | 0 | - |
| Chemo alone | 0 | 1 | - |
| 0.02 | 3.4 | 1.3 | antagonism |
| 0.2 | 0.71 | 0.028 | synergy |
| 2 | 0.75 | 0.003 | synergy |
| 20 | 0.97 | 0.0004 | synergy |

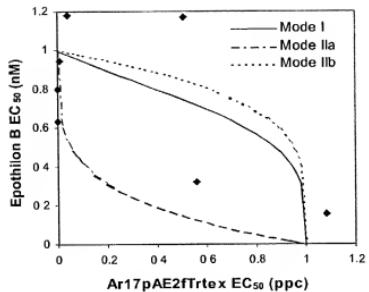


Figure 64

| MR (ppc/nM) | Virus EC ₅₀ ^b | Chemo EC ₅₀ ^b | Effect |
|-------------|-------------------------------------|-------------------------------------|---------|
| Virus alone | 1 | 0 | - |
| Chemo alone | 0 | 1 | - |
| 1.3e-05 | 0.0028 | 0.60 | synergy |
| 5.0e-05 | 0.0078 | 0.42 | synergy |
| 2.0e-04 | 0.029 | 0.39 | synergy |
| 8.0e-04 | 0.11 | 0.36 | synergy |

| MR (ppc/nM) | Virus EC ₅₀ ^b | Chemo EC ₅₀ ^b | Effect |
|-------------|-------------------------------------|-------------------------------------|------------|
| Virus alone | 1 | 0 | - |
| Chemo alone | 0 | 1 | - |
| 1 | 2.2 | 0.015 | antagonism |
| 10 | 0.92 | 6.1e-4 | synergy |
| 100 | 0.34 | 2.2e-5 | synergy |
| 1000 | 0.32 | 2.1e-6 | synergy |



Figure 65

| | Virus
EC ₅₀ ^b | Chemo
EC ₅₀ ^b | Effect |
|-------------|--|--|------------|
| Virus alone | 1 | 0 | - |
| Chemo alone | 0 | 1 | - |
| 3.1e-06 | 0.00045 | 0.63 | synergy |
| 1.3e-05 | 0.0018 | 0.80 | synergy |
| 5.0e-05 | 0.0084 | 0.95 | synergy |
| 2.0e-04 | 0.042 | 1.2 | antagonism |
| 8.0e-04 | 0.18 | 1.6 | antagonism |
| 3.2e-03 | 0.51 | 1.2 | antagonism |
| 1.3e-02 | 0.56 | 0.32 | additivity |
| 5.1e-02 | 1.1 | 0.06 | antagonism |



Figure 66

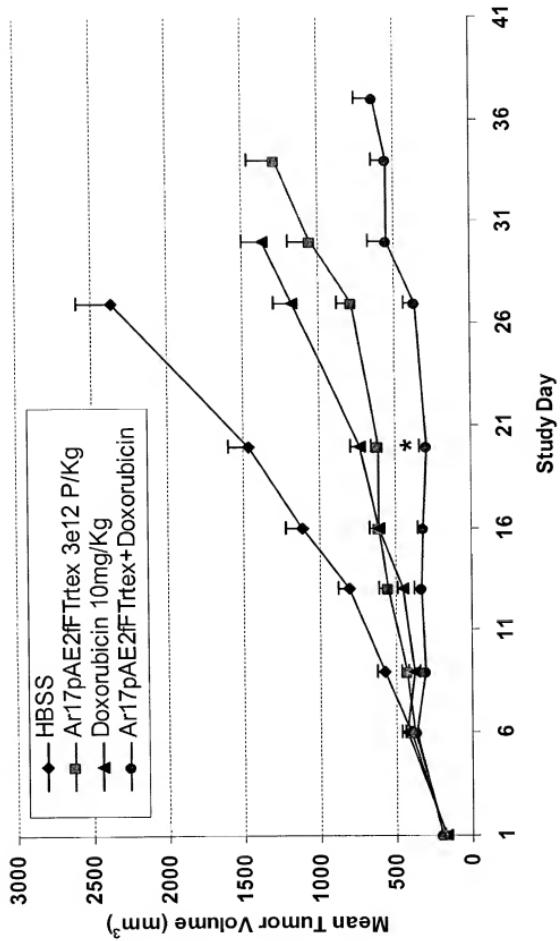


Figure 67

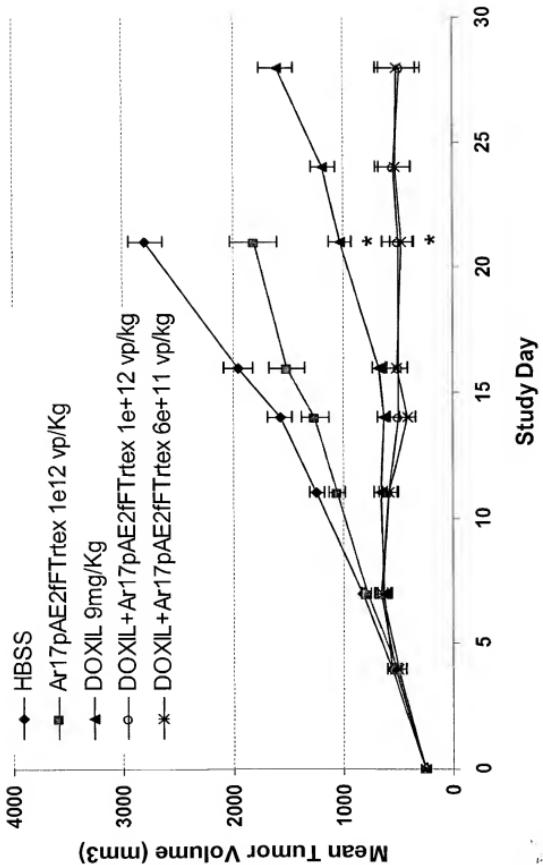


Figure 68

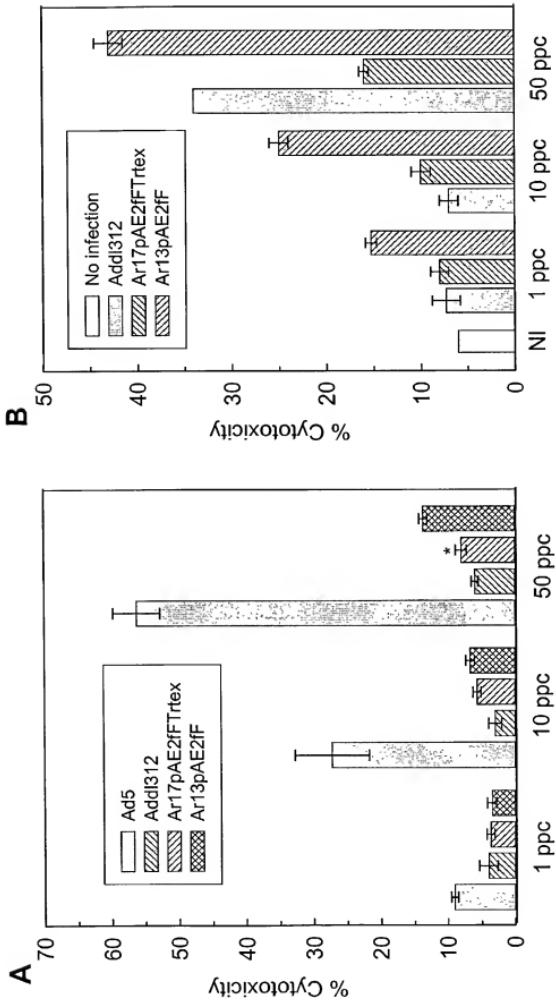


Figure 69

Ad35-Based Oncolytic Vectors

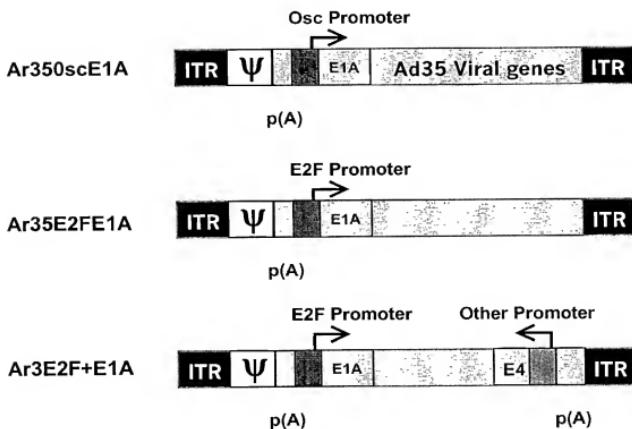


Figure 70

